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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.



**WO 02/077278 A1**

## UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

### TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

### BACKGROUND ART

A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy<sup>1-66</sup>. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (<http://www.ncbi.nlm.nih.gov>) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species.

Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals<sup>67</sup>. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics<sup>68</sup> blood heam analysis<sup>69,70</sup> etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification<sup>71</sup>, Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity<sup>72,73</sup>. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics, therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for forensic wildlife identification.

### **OBJECTS OF THE INVENTION**

The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonably doubt.

Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wantonly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECULAR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

## 15 SUMMARY OF THE INVENTION

Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

## DETAILED DESCRIPTION OF THE INVENTION

20 Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). These sequences were aligned using the software *Clustal X(1.8)*(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (\*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatacatcggtacaaacctagtaga  
 atgaatctgaggagggtctcagtagataaagcaacccttaccggatttttcgccttccactttatctcccatttatcattgcagccctt  
 accatagtacacctactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaattccattccac  
 ccctactacacatatcaaagatatcctaggagctctactattaatttaaccctcatgcttctagtcctattctcaccggacctgcttggag  
 5 accagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgcaatcct  
 ccgatcaattcctaacaaactaggagg”.

A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as ‘mcb398’ and ‘mcb869’ because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398  
 10 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3’ end are highly conserved amongst a vast range of animal  
 15 species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 7d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate  
 20 amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers ‘mcb398’ and ‘mcb869’ invented by the applicants fulfill the objectives of invention.

25 Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using ‘BLAST software’<sup>73</sup>, it indicates identity of the family, genus or species of the analyzed  
 30 material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers ‘mcb398’ and ‘mcb869’. The complete procedure involved in the *analyses* (the word, ‘analyses’ should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading 'Objectives of invention') is briefed under 'Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

#### BRIEF DESCRIPTION OF DRAWING AND TABLES

5 **Figure 1a.** Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. 'adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin 'adil.flesh' was subjected to DNA isolation using the standard procedures<sup>74</sup>. The DNA obtained was amplified using the primers  
10 'mcb398' and 'mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane 'M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from 'adil.flesh' using primers 'mcb398' and 'mcb869'. The PCR amplicon obtained were  
15 sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Biosystems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from 'adil.flesh'.

**Figure 1b.** Illustrates the further steps involved in *analyses*. The sequence (328 bp)  
20 revealed from 'adil.flesh' was subjected to homology search in *nr* (i.e. non-redundant) database of National Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis  
25 revealed the highest homology of the sequence revealed from 'adil.flesh' with the sequence of *Panthera pardus* (gene bank registration number 'AY005809'), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of  
30 'adil.flesh' is similar to the sequences of 'gz1L' further confirming the identity of the source of confiscated remain 'adil.flesh' as that of a *Panthera pardus* origin.

**Figure 1c** illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from 'adil.flesh' and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard '*Panthera pardus*') indicating the identity of the species of 'adil.flesh' as that of a *Panthera pardus* source.

5 **Figure 2** shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:

Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.

10 Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal origin 'i.e. adil.flesh'

Lane 23: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

**Figure 3.** Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:

15 Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

20 **Figure 4.** Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal species. Description of different lanes shown is as follows:

Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.

Lane 24: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

25 **Table 1.** List of 221 animal species used for *In-silico* analysis to design the universal primers 'mcb398' and 'mcb869'. Table also demonstrate the 'P,S scores' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:

Symbol (#) refers to Number

30 Symbol (\*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species  
Symbol (<sup>s</sup>P,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by *Amplify (1.2)* software.

Symbol ( $\overline{P}$ ,S/R) refers to Probability of match and Stability of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify (1.2)* software.

5 **Table 2.** Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (\*) refers to the nucleotide bases which are conserved amongst 221 animal species  
10 listed in Table 1). The alignments have been done using software *CLUSTAL X (1.8)*. The nucleotide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

**Table 3.** Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'mito' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *felis catus* cytochrome b gene sequence (genbank registration number NC\_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements  
15 of column 6 mention above under sub-heading 'Objectives of invention'.

**Table 4.** Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'nr' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *Panthera pardus* cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170)  
25 registered in NCBI database. It gives an indication that the species of analyzed material belongs to *Panthera pardus* origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

**Table 5.** Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in  
30 Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

**Table 6** Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (\*) mark:



however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers  
5 'mcb398' and 'mcb869'.

**Table 7** (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (\*) symbol in Table 6), amongst the 328 bp fragment  
10 revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil.flesh" at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard  
15 '*Panthera pardus*' source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard '*Panthera pardus*' source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis<sup>75</sup>;  
20 however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

**Table 8.** Percent similarity matrix calculated by pair-wise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The  
30 similarity matrix has been calculated using the software *PHYLIP* (3.5).

**Table 9.** Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

**Table 10.** BLAST analysis of primers 'mcb398' in *nr* database of NCBI. It demonstrates

that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer

**Table 11.** BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates

5 that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

**Table 12.** Other animal belonging to distantly related animal species, investigated to

10 confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population

15 of a particular species according to its demographic distributions<sup>75</sup>. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI<sup>1-65</sup>. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small

20 fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by

25 aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in Table 1. These sequences are publicly available in NCBI DNA databases. These sequences were aligned using the software *CLUSTAL X* (1.8). As mentioned before, the 472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the

30 nucleotides between 398 to 869 in *Antelope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (\*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering *Antilope cervicapra* as a representative species, and the sequence the above fragment of cytochrome b gene of *Antilope cervicapra* is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatacatcggtacaaacctagtaga  
 5 atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgccttcactttatcctcccattatcattgcagccctt  
 accatagtagacactactgtttctccacgaaacaggatccaacaacccccacaggaatctcatcagacgcagacaaaaatccaticcac  
 ccctactacactatcaaagatatcctaggagctctactattaatttaaacctcatgcttctagtctctattctcaccggacctgcttgag  
 accagacaactatacaccagcaaaccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgcgaatcct  
 ccgatcaattcctaacaaactaggagg

10 Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972). These species are marked  
 15 with symbol (\*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name	Sequence (5'-3')
20 'mcb398'	“TACCATGAGGACAAATATCATTCTG”
'mcb869'	“CCTCCTAGTTTGTTAGGGATTGATCG”

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico* (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the  
 25 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually. . We assigned the P,S score (P=Probability of  
 30 match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template):

however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were

5 *Eumeces egregius* and *Equus ainus*. *Eumeces egregius* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S

10 score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'tagtagaatgaatctgaggagg3' and AFR=5'atgcaaataggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed

15 in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregius*) for our primers 'mcb398' and 'mcb869',

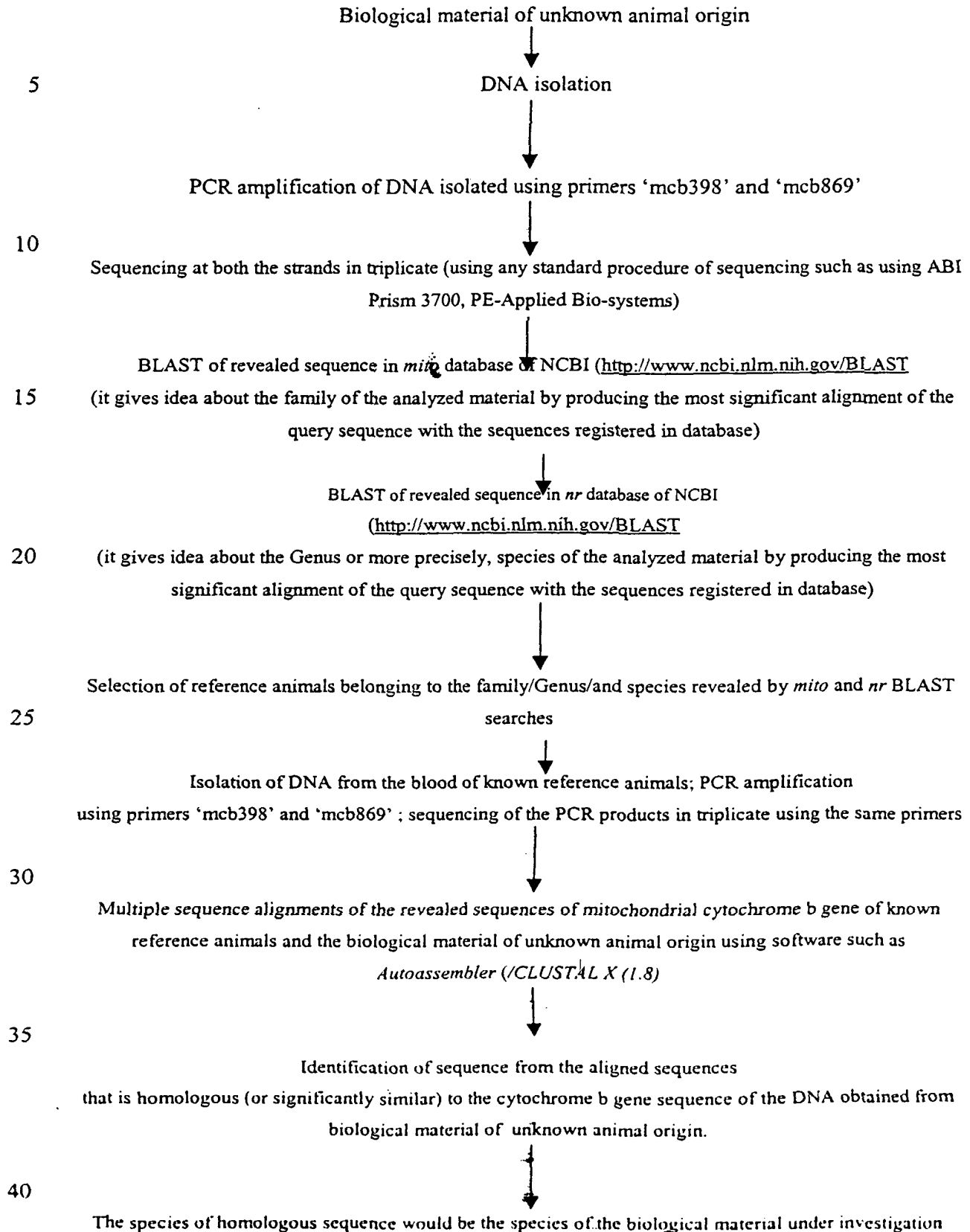
20 respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregius* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb

25 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

30 Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398' and 'mcb 869' are universal primers.

The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'



## Examples

### Example 1

Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading  
5 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies. Being a slow evolving gene, It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources<sup>1-65</sup>. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the *nr*  
10 and *mito* databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species  
15 with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated from any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using  
20 software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). The aligned data was examined carefully for the conserved sites amongst all the species included in *in-silico* analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

25 As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions marked as star (\*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are  
30 characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatatcatcggtacaaacctagtaga  
 atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgcttcactttatcctcccatttatcattgcagccctt  
 accatagtacactactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaaattccattccac  
 ccctactacactatcaaagatactcctaggagctctactattaatttaacccctcatgcttctagtctctattctcaccggacctgcttgag  
 5 accagacaactatacaccagcaaacccttaatacacccccacatatcaagcccgatgatacttctatttgcatagcgaatcct  
 ccgatcaattcctaacaaactaggagg”

### Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under ‘Example 1’.

A pair of universal primer was designed which has the following features:

1. It targets the fragment identified (mentioned under ‘Example 1’) to amplify it in polymerase chain reaction (PCR).
2. Its 3’ and 5’ ends that are highly conserved (marked as star (\*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
3. The  $t_m$  (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer *would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.*
5. The 3’ end of the primers were ensured to have either ‘G’ or ‘C’ to increase the probability of strong bonding at its 3’ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.

8. The sequences of the universal primers invented are as follows:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTTGTTAGGGATTGATCG"

### Example 3:

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the technique invented by us

The PCR conditions developed had the following unique features:

- 1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.
- 20 2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.
3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.
- 25 4. The universal conditions mentioned above are:

Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl<sub>2</sub>, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35<sup>th</sup> cycles should be held for 10 min.



**Example 4:**

Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software *CLUSTAL X* (1.8). The region of cytochrome b gene that was most conserved amongst 221 animal species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (\*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three hydrogen bonds while pairing with each other. The strong bonding at 3' ends helps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop or primer dimer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from *In-silico* analysis :

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b gene

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (\*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico*. In the aligned sequences, the conserved nucleotides are marked with symbol (\*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually.

(b) P, S, score analysis:

We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were *Eumeces egregius* and *Equus ainus*. *Eumeces egregius* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'ctagtagaatgaatctgaggagg<sup>5</sup> and AFR= 5'tatgcaaataaggaagtatcattc<sup>3</sup>.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregius*) for our primers 'mcb398' and 'mcb869', respectively, were higher than the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregius* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

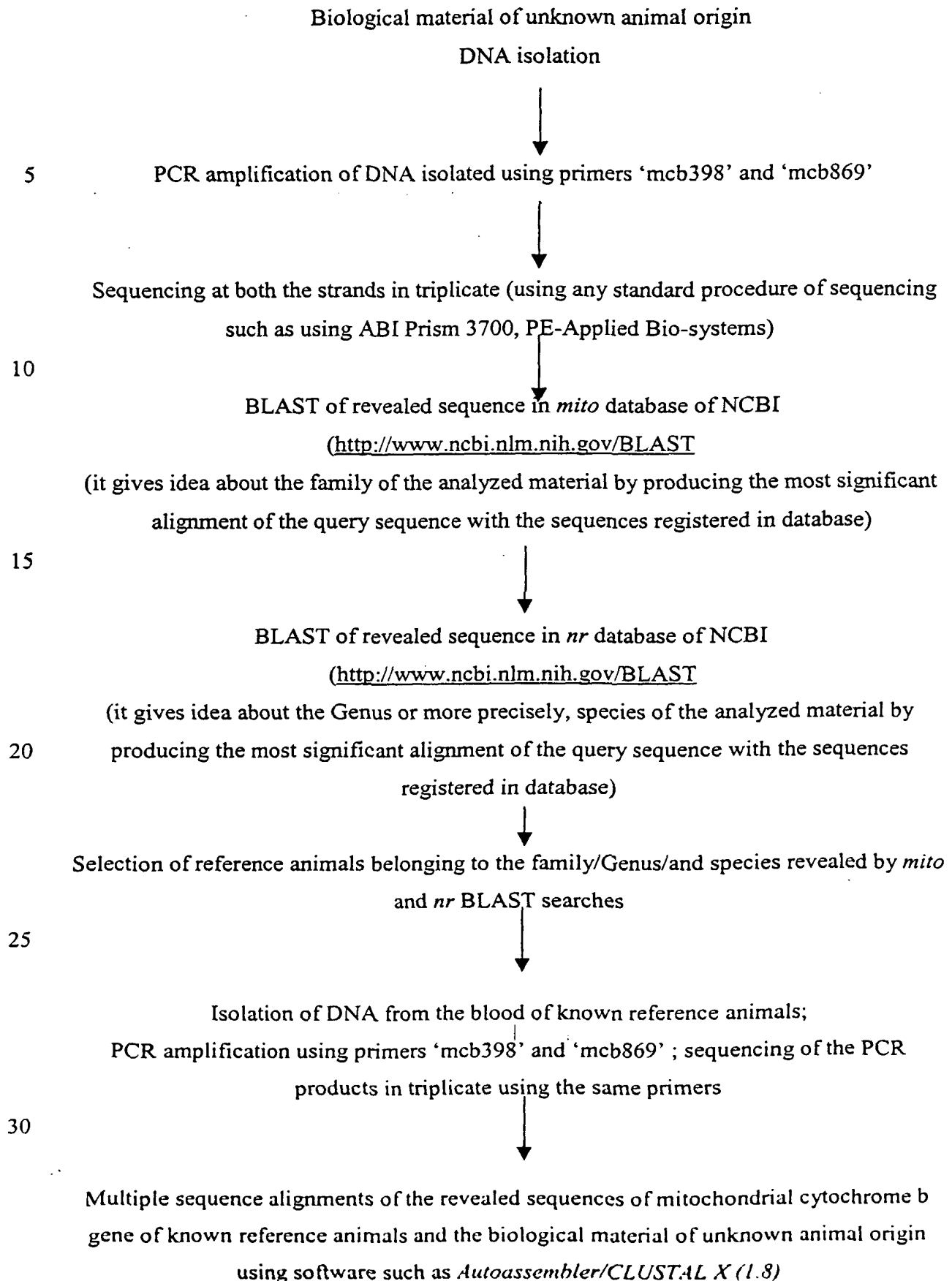
(2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869'. The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.

**Example 5:**

Example to establish the identity of confiscated remains from unknown animal origin using the universal primers 'mcb398' and 'mcb869'.

The step-wise procedure to establish the identity of the biological material from an unknown animal source is mentioned below:





Identification of sequence from the aligned sequences  
that is homologous (or significantly similar) to the cytochrome b gene sequence of the  
5 DNA obtained from biological material of  
unknown animal origin.



10 The species of homologous sequence would be the species of the biological material under  
investigation



Application of the above information for the objectives mentioned in columns 7-13 under  
sub-heading 'Objective of invention' of heading 'Summary of invention'

15 **Example 6:**

The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we  
investigated a case of forensic identification submitted at our laboratory to seek scientific  
opinion on animal hunting evidence. In this case, we received the half burned remains of  
20 an unknown animal, confiscated by the crime investigation agencies. The DNA was  
isolated from the above material following standard methods<sup>74</sup> and subjected to PCR  
amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869').  
Amplification reactions were carried out in 20 µl reaction volume containing 20 ng of  
template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl<sub>2</sub>, 0.5 unit  
25 of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer  
(10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an  
initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C  
for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step  
at 35<sup>th</sup> cycles was held for 10 min.

30 The PCR products obtained were sequenced in automated work station (ABI Prism 3700,  
PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in  
Figure 1a) was blasted against *mito* databases of NCBI using BLAST program<sup>73</sup>. The most  
significant alignment (bits Value 365, E value  $e^{-101}$ ) of this sequence was produced with  
the cytochrome b gene sequence of *Felis catus*, (Table 3) indicating that species of

analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against *nr* databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value  $e^{-170}$ ) of this sequence was produced with the cytochrome b gene sequence of *Panthera pardus* (Table 4), indicating the identity of the analyzed material as that of a *Panthera pardus* source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program *CLUSTAL X (1.8)* (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-wise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by a their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 demonstrate that the maximum similarity of the adil.flesh with 'gz11' i.e. known Leopard (*Panthera pardus*) species, indicating the identity of the adil.flesh, the confiscated skin, as that of a *Panthera pardus* origin. We also calculated the similarity matrix showing the pair-wise similarity amongst the animal species under investigation using *PHYLIP* software. This matrix is shown in Table 8. It demonstrates that the animals belonging to different species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source (99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (*Panthera pardus*) species. The step-wise procedure involved in above analysis is illustrated in Figure 1a, 1b and 1c, respectively.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software<sup>73</sup>, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have identified a fragment on the mitochondrial cytochrome b gene, which has enormous information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for *in-silico* analysis

SN. Code	Name	NCBI accession #	<sup>†</sup> P,S/F	<sup>‡</sup> P,S/R
1 aep.mel	<i>Aepyceros melampus</i>	AF036289 <sup>1</sup>	97, 60	94, 62
2 ore.ore	<i>Oreotragus oreotragus</i>	AF036283 <sup>1</sup>	88, 52	94, 62
3 add.nas	<i>Addax nasomaculatus</i>	AF034722 <sup>2</sup>	97, 60	95, 66
4 ory.dam	<i>Oryx damah</i>	AJ222685 <sup>1</sup>	90, 58	95, 66
5 hip.equ	<i>Hippotragus equinus</i>	AF022060 <sup>3</sup>	98, 63	85, 55
6 alc.bus	<i>Alcelaphus buselaphus</i>	AJ222681 <sup>1</sup>	97, 60	98, 68
7 sig.lic	<i>Sigmoceros lichtensteinii</i>	AF034967 <sup>4</sup>	97, 60	98, 68
8 bea.hun	<i>Beatragus hunteri</i>	AF034968 <sup>4</sup>	97, 60	94, 62
9 dam.lun	<i>Damaliscus lunatus</i>	AF016635 <sup>3</sup>	97, 60	77, 55
10 con.tau	<i>Connochaetes taurinus</i>	AF016638 <sup>3</sup>	82, 56	93, 62
11 bis.bon	<i>Bison bonasus</i>	Y15005 <sup>5</sup>	90, 58	87, 63
12 bos.gru	<i>Bos grunniens</i> *	AF091631 <sup>6</sup>	90, 58	94, 62
13 bos.tra	<i>Bos tragocamelus</i> *	AJ222679 <sup>1</sup>	90, 58	95, 66
14 buba.bub	<i>Bubalus bubalis</i> *	D34637 <sup>7</sup>	97, 60	93, 64
15 bub.min	<i>Bubalus mindorensis</i>	D82895 <sup>8</sup>	97, 60	87, 62
16 tra.ang	<i>Tragelaphus angasii</i>	AF091633 <sup>6</sup>	97, 60	87, 63
17 tra.eur	<i>Tragelaphus eurycerus</i>	AF036276 <sup>1</sup>	90, 58	97, 64
18 nem.cau	<i>Nemorhaedus caudatus</i> *	U17861 <sup>9</sup>	95, 61	93, 59
19 pse.nay	<i>Pseudois nayaur</i>	AF034732 <sup>2</sup>	89, 55	89, 59
20 amm.ler	<i>Ammotragus lervia</i>	AF034731 <sup>2</sup>	94, 58	97, 63
21 cap.fal	<i>Capra falconeri</i> *	D84202 <sup>10</sup>	98, 63	95, 66
22 cap.ibe	<i>Capra ibex</i> *	AF034735 <sup>2</sup>	98, 63	89, 58
23 hem.jem	<i>Hemitragus jemlahicus</i> *	AF034733 <sup>2</sup>	95, 61	90, 61
24 rup.pyr	<i>Rupicapra pyrenaica</i>	AF034726 <sup>2</sup>	95, 61	89, 59
25 rup.rup	<i>Rupicapra rupicapra</i>	AF034725 <sup>2</sup>	95, 61	94, 64
26 pan.hod	<i>Pantholops hodgsoni</i>	AF034724 <sup>2</sup>	98, 63	95, 66
27 bud.tax.tax	<i>Budorcas taxicolor taxicolor</i> *	U17868 <sup>9</sup>	90, 58	95, 66
28 ovi.amm	<i>Ovis ammon</i> *	AF034727 <sup>2</sup>	98, 63	97, 64
29 ovi.vig	<i>Ovis vignei</i> *	AF034729 <sup>2</sup>	98, 63	97, 64
30 cap.cri	<i>Capicornis crispus</i> *	AJ304502 <sup>11</sup>	98, 63	94, 63
31 ovi.mos	<i>Ovibos moschatus</i>	U17862 <sup>9</sup>	98, 63	92, 61
32 ore.ame	<i>Oreamnos americanus</i>	AF190632 <sup>12</sup>	98, 63	94, 62
33 cep.dor	<i>Cephalophus dorsalis</i>	AF091634 <sup>6</sup>	97, 58	90, 61
34 cep.max	<i>Cephalophus maxwellii</i>	AF096629 <sup>13</sup>	97, 60	88, 53
35 alc.alc	<i>Alces alces</i>	AJ000026 <sup>14</sup>	95, 61	93, 59
36 hyd.ine	<i>Hydropotes inermis</i>	AJ000028 <sup>14</sup>	97, 60	90, 63
37 mun.mun	<i>Muntiacus muntjak</i> *	AF042713 <sup>15</sup>	90, 58	93, 64
38 cer.ele.kan	<i>Cervus elaphus kansuensis</i> *	AB021098 <sup>16</sup>	98, 63	82, 59
39 cer.ele.xan	<i>Cervus elaphus xanthopygus</i> *	AB021097 <sup>16</sup>	98, 63	82, 59
40 cer.ele.can	<i>Cervus elaphus canadensis</i> *	AB021096 <sup>16</sup>	98, 63	90, 61
41 cer.nip.ce	<i>Cervus nippon centralis</i>	AB021094 <sup>16</sup>	98, 63	90, 61
42 cer.nip.ye	<i>Cervus nippon yesoensis</i>	AB021095 <sup>16</sup>	98, 63	90, 61
43 cer.nip.ke	<i>Cervus nippon keramuc</i>	AB021091 <sup>16</sup>	98, 63	90, 61



44	cer.nip.pu	<i>Cervus nippon pulchellus</i>	AB021090 <sup>16</sup>	98, 63	90, 61
45	cer.nip.ni	<i>Cervus nippon nippon</i>	AB021093 <sup>16</sup>	98, 63	90, 61
46	cer.ela.sc	<i>Cervus elaphus scoticus</i>	AB021099 <sup>16</sup>	98, 63	90, 61
47	cer.dam	<i>Cervus dama</i>	AJ000022 <sup>14</sup>	98, 63	88, 53
48	ran.tar	<i>Rangifer tarandus</i>	AJ000029 <sup>14</sup>	98, 63	89, 57
49	mos.fus	<i>Moschus fuscus</i> *	AF026888 <sup>17</sup>	90, 59	90, 61
50	mos.leu	<i>Moschus leucogaster</i> *	AF026889 <sup>17</sup>	90, 59	90, 61
51	mos.chr	<i>Moschus chrysogaster</i> *	AF026887 <sup>17</sup>	90, 59	90, 61
52	mos.ber	<i>Moschus berezovskii</i> *	AF026886 <sup>17</sup>	90, 59	90, 61
53	mos.mos	<i>Moschus moschiferus</i> *	AF026883 <sup>17</sup>	90, 59	92, 61
54	kob.ell	<i>Kobus ellipsiprymnus</i>	AF022059 <sup>3</sup>	91, 61	95, 66
55	kob.meg	<i>Kobus megaceros</i>	AJ222686 <sup>1</sup>	91, 61	83, 56
56	red.aru	<i>Redunca arundinum</i>	AF096628 <sup>13</sup>	91, 61	94, 62
57	red.ful	<i>Redunca fulvorufula</i>	AF036284 <sup>1</sup>	89, 57	94, 62
58	neo.mos	<i>Neotragus moschatus</i>	AJ222683 <sup>1</sup>	89, 57	94, 62
59	pel.cap	<i>Pelea capreolus</i>	AF022055 <sup>3</sup>	91, 61	90, 61
60	ant.cer	<i>Antilope cervicapra</i> *	AF022058 <sup>3</sup>	82, 56	93, 64
61	sai.tat	<i>Saiga tatarica</i>	AF064487 <sup>18</sup>	91, 61	92, 61
62	gaz.dam	<i>Gazella dama</i>	AF025954 <sup>3</sup>	91, 61	92, 61
63	our.our	<i>Ourebia ourebi</i>	AF036288 <sup>1</sup>	82, 56	82, 59
64	gaz.gaz	<i>Gazella gazella</i> *	AJ222682 <sup>1</sup>	91, 61	89, 57
65	rap.mel	<i>Raphicerus melanotis</i>	AF022053 <sup>3</sup>	81, 54	80, 50
66	mad.kir	<i>Madoqua kirkii</i>	AF022070 <sup>3</sup>	90, 58	97, 65
67	ant.ame	<i>Antilocapra americana</i>	AF091629 <sup>6</sup>	98, 63	98, 68
68	tra.jav	<i>Tragulus javanicus</i> *	D32189 <sup>19</sup>	86, 57	86, 59
69	tra.nap	<i>Tragulus napu</i> *	X56288 <sup>20</sup>	81, 52	93, 58
70	bal.acu	<i>Balaenoptera acutorostrata</i>	X75753 <sup>21</sup>	89, 56	97, 61
71	bal.bon	<i>Balaenoptera bonaerensis</i>	X75581 <sup>21</sup>	89, 56	93, 59
72	bal.bor	<i>Balaenoptera borealis</i> *	X75582 <sup>21</sup>	89, 56	93, 59
73	bal.edi	<i>Balaenoptera edeni</i>	X75583 <sup>21</sup>	89, 56	88, 54
74	esc.rob	<i>Eschrichtius robustus</i> *	X75585 <sup>21</sup>	97, 61	86, 57
75	bal.mus	<i>Balaenoptera musculus</i> *	NC_001601 <sup>22</sup>	97, 57	93, 59
76	meg.nov	<i>Megaptera novaeangliae</i> *	X75584 <sup>21</sup>	97, 61	94, 63
77	bal.phy	<i>Balaenoptera physalus</i> *	NC_001321 <sup>23</sup>	97, 57	94, 63
78	cap.mar	<i>Caperea marginata</i>	X75586 <sup>21</sup>	93, 55	91, 53
79	cep.com	<i>Cephalorhynchus commersonii</i>	AF084073 <sup>24</sup>	85, 51	88, 55
80	cep.eut	<i>Cephalorhynchus eutropia</i> *	AF084072 <sup>24</sup>	85, 51	92, 59
81	lag.obl	<i>Lagenorhynchus obliquidens</i>	AF084067 <sup>24</sup>	94, 59	92, 59
82	cep.hez	<i>Cephalorhynchus heavisidii</i>	AF084070 <sup>24</sup>	89, 56	97, 63
83	cep.hec	<i>cephalorhynchus hectori</i> *	AF084071 <sup>24</sup>	89, 56	92, 59
84	lag.aus	<i>Lagenorhynchus australis</i>	AF084069 <sup>24</sup>	86, 54	92, 59
85	lag.cru	<i>Lagenorhynchus cruciger</i>	AF084068 <sup>24</sup>	86, 54	92, 59
86	lag.obs	<i>Lagenorhynchus obscurus</i>	AF084066 <sup>24</sup>	86, 54	92, 59
87	lis.bor	<i>Lissodelphis borealis</i>	AF084064 <sup>24</sup>	85, 51	92, 59
88	lis.per	<i>Lissodelphis peronii</i>	AF084065 <sup>24</sup>	86, 54	92, 59
89	glo.mac	<i>Globicephala macrorhynchus</i>	AF084055 <sup>24</sup>	94, 59	88, 55
90	glo.mel	<i>Globicephala melas</i>	AF084056 <sup>24</sup>	94, 59	88, 55
91	fer.att	<i>Feresa attenuata</i> *	AF084052 <sup>24</sup>	94, 59	92, 59

92	pep.ele	<i>Peponocephala electra</i> *	AF084053 <sup>24</sup>	94, 59	88, 55
93	gra.gri	<i>Grampus griseus</i>	AF084059 <sup>24</sup>	97, 61	89, 59
94	pse.cra	<i>Pseudorca crassidens</i> *	AF084057 <sup>24</sup>	94, 59	92, 59
95	lag.acu	<i>Lagenorhynchus acutus</i>	AF084075 <sup>24</sup>	98, 63	89, 59
96	orci.bre	<i>Orcinus orca</i>	AF084061 <sup>24</sup>	86, 57	82, 52
97	orca.bre	<i>Orcaella brevirostris</i>	AF084063 <sup>24</sup>	86, 57	91, 54
98	del.cap	<i>Delphinus capensis</i>	AF084087 <sup>24</sup>	96, 54	97, 63
99	del.tro	<i>Delphinus tropicalis</i>	AF084088 <sup>24</sup>	97, 57	97, 63
100	del.del	<i>Delphinus delphis</i>	AF084085 <sup>24</sup>	97, 57	97, 63
101	sten.cly	<i>Stenella clymene</i>	AF084083 <sup>24</sup>	97, 57	97, 63
102	sten.coe	<i>Stenella coeruleoalba</i>	AF084082 <sup>24</sup>	97, 57	97, 66
103	tur.adu	<i>Tursiops aduncus</i>	AF084092 <sup>24</sup>	97, 57	97, 63
104	sten.fro	<i>Stenella frontalis</i>	AF084090 <sup>24</sup>	97, 57	97, 63
105	saus.chi	<i>Sousa chinensis</i>	AF084080 <sup>24</sup>	97, 57	88, 59
106	sten.lon	<i>Stenella longirostris</i>	AF084103 <sup>24</sup>	97, 61	97, 63
107	turs.tru	<i>Tursiops truncatus</i>	AF084095 <sup>24</sup>	97, 57	96, 59
108	lage.alb	<i>Lagenorhynchus alborostris</i>	AF084074 <sup>24</sup>	97, 61	97, 66
109	sten.bre	<i>Steno bredanensis</i>	AF084077 <sup>24</sup>	97, 61	94, 64
110	sota.flu	<i>Sotalia fluviatilis</i>	AF304067 <sup>25</sup>	97, 61	97, 63
111	del.leu	<i>Delphinapterus leucas</i>	U72037 <sup>26</sup>	97, 61	95, 66
112	mono.mon	<i>Monodon monoceros</i>	U72038 <sup>26</sup>	97, 61	95, 66
113	plat.gan	<i>Platanista gangetica</i> *	AF304070 <sup>25</sup>	97, 61	86, 59
114	plat.min	<i>Platanista minor</i> *	X92543 <sup>27</sup>	97, 61	86, 59
115	kogi.bre	<i>Kogia breviceps</i>	U72040 <sup>26</sup>	97, 59	90, 63
116	kogi.sim	<i>Kogia simus</i>	AF304072 <sup>25</sup>	96, 55	92, 63
117	phys.cat	<i>Physeter catodon</i>	AF304073 <sup>25</sup>	97, 57	80, 58
118	lipo.vex	<i>Lipotes vexillifer</i> *	AF304071 <sup>25</sup>	89, 56	83, 53
119	phoc.sin	<i>phocoena sinus</i>	AF084051 <sup>24</sup>	87, 49	92, 62
120	bera.bai	<i>Berardius bairdii</i>	X92541 <sup>27</sup>	96, 55	90, 59
121	ziph.car	<i>Ziphius cavirostris</i>	X92540 <sup>27</sup>	97, 61	89, 57
122	meso.eur	<i>Mesoplodon europaeus</i>	X92537 <sup>27</sup>	97, 57	90, 61
123	meso.bid	<i>Mesoplodon bidens</i>	X92538 <sup>27</sup>	97, 61	92, 61
124	meso.den	<i>Mesoplodon densirostris</i>	X92536 <sup>27</sup>	91, 61	94, 63
125	hype.amp	<i>Hyperoodon ampullatus</i> *	X92539 <sup>27</sup>	97, 61	90, 65
126	meso.per	<i>Mesoplodon peruvianus</i>	AF304074 <sup>25</sup>	97, 61	86, 58
127	pont.bla	<i>Pontoporia blainvillei</i>	AF304069 <sup>25</sup>	92, 59	88, 55
128	hipp.amp	<i>Hippopotamus amphibius</i>	Y08813 <sup>29</sup>	92, 58	95, 66
129	hex.lib	<i>Hexaprotodon liberiensis</i>	Y08814 <sup>29</sup>	98, 63	97, 66
130	rhin.son	<i>Rhinoceros sondaicus</i> *	AJ245725 <sup>10</sup>	90, 59	87, 61
131	cera	<i>Ceratotherium simum</i>	NC_001808 <sup>12</sup>	90, 59	90, 63
132	dic.sum	<i>Dicerorhinus sumatrensis</i>	AJ245723 <sup>10</sup>	90, 59	86, 57
133	equu	<i>Equus asinus</i>	NC_001788 <sup>11</sup>	91, 61	73, 51
134	baby.bab	<i>Babyrousa babyrussa</i>	Z50106 <sup>11</sup>	89, 56	85, 56
135	phac.afri	<i>Phacochoerus africanus</i>	Z50090 <sup>11</sup>	90, 59	87, 54
136	sus.scr.ew	<i>Sus scrofa haplotype EWBj</i> *	AF136549 <sup>14</sup>	97, 57	83, 54
137	sus.bar	<i>Sus barbatus</i>	Z50107 <sup>11</sup>	97, 57	85, 55
138	lama.gla	<i>Lama glama</i>	U06429 <sup>11</sup>	89, 55	85, 53
139	lama.gua	<i>Lama guanicoe</i>	Y08812 <sup>29</sup>	88, 54	86, 57

140 vic.vic	<i>Vicugna vicugna</i>	U06430 <sup>35</sup>	89, 55	85, 53
141 cam.bac	<i>Camelus bactrianus</i>	U06427 <sup>35</sup>	94, 58	86, 58
142 arc.for	<i>Arctocepalus forsteri</i>	XS2293 <sup>36</sup>	97, 60	87, 64
143 arc.gaz	<i>Arctocepalus gazella</i>	X82292 <sup>36</sup>	94, 58	87, 64
144 eum.jub	<i>Eumetopias jubatus</i>	X82311 <sup>36</sup>	97, 57	86, 57
145 zal.cal	<i>Zalophus californianus</i>	XS2310 <sup>36</sup>	89, 55	86, 57
146 odo.ros	<i>Odobenus rosmarus</i>	X82299 <sup>36</sup>	91, 61	81, 52
147 pho.vit	<i>Phoca vitulina</i>	X82306 <sup>36</sup>	90, 58	87, 64
148 pho.fascia	<i>Phoca fasciata</i>	XS2302 <sup>36</sup>	98, 63	95, 66
149 pho.gro	<i>Phoca groenlandica</i>	X82303 <sup>36</sup>	92, 59	90, 61
150 cys.cri	<i>Cystophora cristata</i>	X82294 <sup>36</sup>	89, 56	87, 64
151 hyd.lep	<i>Hydrurga leptonyx</i>	X82297 <sup>36</sup>	89, 55	82, 54
152 lep.wed	<i>Leptonychotes weddelli</i>	X72005 <sup>37</sup>	98, 63	91, 66
153 mir.leo	<i>Mirounga leonina</i>	X82298 <sup>36</sup>	89, 55	82, 59
154 eri.bar	<i>Erignathus barbatus</i>	X82295 <sup>36</sup>	89, 56	87, 63
155 mon.sch	<i>Monachus schauinslandi</i>	X72209 <sup>37</sup>	91, 61	87, 60
156 hela.mal	<i>Helarctos malayanus</i> *	U18399 <sup>38</sup>	84, 54	90, 63
157 sel.thi	<i>Selenarctos thibetanus</i> *	AB020910 <sup>39</sup>	89, 57	87, 64
158 ail.ful	<i>Ailurus fulgens</i> *	X94919 <sup>40</sup>	93, 55	87, 64
159 fel	<i>Felis catus</i>	NC_001700 <sup>41</sup>	85, 56	90, 63
160 can	<i>Canis familiaris</i>	NC_002008 <sup>42</sup>	98, 58	84, 54
161 tal	<i>Talpa europaea</i>	NC_002391 <sup>43</sup>	81, 50	92, 57
162 gla.sab	<i>Glaucornys sabrinus</i>	AF011738 <sup>44</sup>	90, 59	82, 54
163 gla.vol	<i>Glaucornys volans</i>	AB030261 <sup>45</sup>	90, 59	87, 60
164 hyl.pha	<i>Hylopotes phayrei</i> *	AB030259 <sup>45</sup>	91, 61	81, 50
165 pet.set	<i>Petionomys setosus</i> *	AB030260 <sup>45</sup>	91, 61	81, 50
166 bel.pea	<i>Belomys pearsonii</i> *	AB030262 <sup>45</sup>	91, 61	87, 64
167 pte.mom	<i>Pteromys momonga</i> *	AB030263 <sup>45</sup>	97, 61	90, 63
168 gala.demi	<i>Galagoides demidoff</i>	AF271411 <sup>46</sup>	97, 58	87, 64
169 pero.pot	<i>Perodicticus potto</i>	AF271413 <sup>46</sup>	97, 60	87, 63
170 gala.mat	<i>Galago matschiei</i>	AF271409 <sup>46</sup>	97, 60	90, 61
171 gala.moh	<i>Galago moholi</i>	AF271410 <sup>46</sup>	97, 57	95, 66
172 oto.gar	<i>Otolemur garnettii</i>	AF271412 <sup>46</sup>	92, 58	87, 60
173 lor.tar	<i>Loris tardigradus</i> *	US3581 <sup>47</sup>	97, 60	93, 59
174 nyc.cou	<i>Nycticebus coucang</i> *	US3580 <sup>47</sup>	97, 60	95, 66
175 mus	<i>Mus musculus</i>	NC_001569 <sup>48</sup>	97, 60	86, 59
176 gor	<i>Gorilla gorilla</i>	NC_001645 <sup>49</sup>	89, 57	80, 58
177 homo	<i>Homo sapiens sapiens</i>	NC_001807 <sup>50</sup>	96, 55	84, 64
178 dug.dug	<i>Dugong dugong</i> *	U07564 <sup>51</sup>	97, 60	89, 59
179 ele.max	<i>Elephas maximus</i> *	AB002412 <sup>52</sup>	97, 60	76, 57
180 afr.con	<i>Afropavo congensis</i>	AF013760 <sup>53</sup>	97, 58	87, 63
181 pavo.mut	<i>Pavo muticus</i> *	AF013763 <sup>53</sup>	97, 57	87, 63
182 tra.bly	<i>Tragopan blythii</i> *	AF200722 <sup>54</sup>	89, 55	85, 57
183 tra.sat	<i>Tragopan satyra</i> *	AF229837 <sup>54</sup>	89, 55	86, 61
184 tra.cob	<i>Tragopan caboti</i>	AF200723 <sup>54</sup>	89, 55	86, 61
185 tra.tem	<i>Tragopan temminckii</i> *	AF023802 <sup>55</sup>	89, 55	81, 56
186 arg.arg	<i>Argusianus argus</i>	AF013761 <sup>55</sup>	89, 55	87, 63
187 cat.wal	<i>Catrcus wallichi</i> *	AF028792 <sup>55</sup>	88, 54	85, 57

188	cro.cro	<i>Crossoptilon crossoptilon</i> *	AF028794 <sup>53</sup>	89, 55	85, 57
189	sym.rec	<i>Syrnaticus reevesi</i> *	AF028801 <sup>53</sup>	89, 55	85, 57
190	bam.tho	<i>Bambusicola thoracica</i> *	AF028790 <sup>53</sup>	80, 48	94, 64
191	fra.fra	<i>Francolinus francolinus</i>	AF013762 <sup>53</sup>	97, 58	86, 61
192	ith.cru	<i>Ithaginis cruentus</i> *	AF068193 <sup>53</sup>	98, 63	85, 57
193	ant.par	<i>Anthropoides paradisca</i>	U27557 <sup>56</sup>	85, 56	82, 58
194	ant.vir	<i>Anthropoides virgo</i>	U27545 <sup>56</sup>	84, 54	82, 52
195	gru.ant.an	<i>Grus antigone antigone</i>	U11060 <sup>57</sup>	90, 53	87, 63
196	gru.ant.gi	<i>Grus antigone gillae</i>	U11064 <sup>57</sup>	90, 53	87, 63
197	gru.any.sh	<i>Grus antigone sharpei</i>	U11061 <sup>57</sup>	90, 53	87, 63
198	gru.leu	<i>Grus leucogeranus</i> *	U27549 <sup>56</sup>	90, 53	87, 63
199	gru.can.pr	<i>Grus canadensis pratensis</i>	U27553 <sup>56</sup>	97, 60	87, 63
200	gru.can.ro	<i>Grus canadensis rowani</i>	U27552 <sup>56</sup>	97, 60	87, 63
201	gru.can.ta	<i>Grus canadensis tabida</i>	U27551 <sup>56</sup>	98, 63	87, 63
202	gru.can.ca	<i>Grus canadensis canadensis</i>	U27554 <sup>56</sup>	97, 61	87, 63
203	gru.ame	<i>Grus americana</i>	U27555 <sup>56</sup>	90, 53	87, 63
204	gru.gru	<i>Grus grus</i>	U27546 <sup>56</sup>	89, 54	87, 63
205	gru.mon	<i>Grus monacha</i> *	U27548 <sup>56</sup>	90, 53	87, 63
206	gru.nig	<i>Grus nigricollis</i> *	U27547 <sup>56</sup>	90, 53	87, 63
207	gru.jap	<i>Grus japonensis</i>	U27550 <sup>56</sup>	81, 54	87, 63
208	cic.boy	<i>Ciconia boyciana</i> *	NC_002196 <sup>58</sup>	94, 58	79, 60
209	rhe.ame	<i>Rhea americana</i>	AF090339 <sup>59</sup>	93, 63	79, 60
210	ant.alb	<i>Anthracoceros albirostris</i> *	U89190 <sup>60</sup>	97, 61	86, 59
211	fal.fam	<i>Falco femoralis</i>	U83310 <sup>61</sup>	97, 61	86, 60
212	fal.ver	<i>Falco verpertinus</i>	U83311 <sup>61</sup>	97, 61	85, 57
213	fal.par	<i>Falco peregrinus</i> *	U83307 <sup>61</sup>	97, 61	84, 52
214	fal.spa	<i>Falco sparverius</i>	U83306 <sup>61</sup>	92, 59	80, 51
215	ayt.ame	<i>Aythya americana</i>	NC_000877 <sup>62</sup>	98, 63	94, 62
216	smi.sha	<i>Smithornis sharpei</i>	NC_000879 <sup>59</sup>	97, 53	90, 61
217	vid.cha	<i>Vidua chalybeata</i>	NC_000880 <sup>59</sup>	97, 60	87, 64
218	chry.pic	<i>Chrysemys picta</i>	NC_002073 <sup>63</sup>	89, 56	86, 57
219	emy.orb.ku	<i>Emys orbicularis</i>	AJ131425 <sup>64</sup>	90, 59	94, 63
220	che.mud	<i>Chelonia mydas</i> *	AB012104 <sup>65</sup>	90, 58	94, 63
221	eum.egr	<i>Eumeces egregius</i>	AB016606 <sup>65</sup>	86, 55	73, 51

Table 2. Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene of 221 animal species

PRIMER 'mcb393'	TACCATGAGGACAAATATCATTCTG	
aep.mel	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACAAATCTCTCTCAGCAA	60
ore.ore	TTCCCTGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACTAATCTCTCTCAGCAA	60
add.nas	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
ory.dam	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTTATCCTAACCCTCTCTCTCAGCAA	60
hip.equ	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
alc.bus	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
sig.lic	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
bea.hun	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
dam.lun	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCCTAACCCTCTCTCTCAGCAA	60
con.tau	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
amm.ler	TGCCATGAGGACAGATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
pse.nay	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
cap.ibe	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
hem.jem	TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
cap.fal	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
rup.pyt	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCTCAGCAA	60
rup.rup	TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTTATTACCAATCTCTCTCAGCAA	60
nem.cau	TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTTATTACCAATCTCTCTCAGCAA	60
bud.tax.tax	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCTCAGCAA	60
pan.hod	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTAAATTACCAACCTCTCTCTCAGCAA	60
ovi.amm	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCTCAGCAA	60
ovi.vig	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCTCAGCAA	60
cap.cri	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACTAACCCTCTCTCTCAGCAA	60
ovi.mos	TACCATGAGGACAAATATCATTCTGAGGAGCTACAGTCATCACCACCTCTCTCTCAGCAA	60
ore.ame	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCTCAGCAA	60
cep.dor	TCCCATGAGGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCTCTCTCAGCAA	60
cep.max	TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCTCTCTCAGCAA	60
bis.bon	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCTCAGCAA	60
bos.gru	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCTCAGCAA	60
bos.tra	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTATTATCAGCAA	60
bub.min	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
buba.bub	TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
tra.ang	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
tra.eur	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
kob.ell	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
kob.meg	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTCATCCTAATCTCTCTCTCAGCAA	60
red.aru	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTTATCCTAATCTCTCTCTCAGCAA	60
red.ful	TGCCATGGGGACAAATATCCTTTCTGAGGAGCAACAGTTATCCTAACCCTCTCTCTCAGCAA	60
neo.mos	TGCCATGGGGACAAATATCCTTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
pel.cap	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
gac.dam	TACCATGAGGACAAATATCCTTTCTGAGGGGGCAACAGTTATCCTAACCCTCTCTCTCAGCAA	60
our.our	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
ant.cer	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
sal.sar	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA	60
mad.kir	TGCCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTTATCCTAACCCTCTCTCTCAGCAA	60
rap.mel	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTCATCCTAATCTCTCTCTCAGCAA	60
gac.gac	TACCATGAGGACAAATATCCTTTCTGAGGAGCAACAGTTATCCTAACCCTCTCTCTCAGCAA	60
ant.ame	TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCCTAACCCTCTCTCTCAGCAA	60
hyd.lne	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCCTAACCCTCTCTCTCAGCAA	60
mun.mun	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCCTAACCCTCTCTCTCAGCAA	60
alc.als	TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTTATTACCAATCTCTCTCTCAGCAA	60
gac.ela.kun	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCTCAGCAA	60

cer.ela.xan	TACCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTTCTCTCAGCAA	60
cer.ela.can	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.nip.cent	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA	60
cer.nip.yes	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA	60
cer.nip.ker	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.nip.pul	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.nip.nip	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA	60
cer.ela.sco	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA	60
cer.dam	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA	60
ran.tar	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATCACAAACCTCCTCTCAGCAA	60
mos.fus	TACCTTGAGGACAAATATCTTTCTGAGGAGCGACAGTTATTACCAATCTTCTCTCAGCAA	60
mos.leu	TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA	60
mos.chr	TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA	60
mos.ber	TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA	60
mos.mos	TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTCATCACTAACCTTCTCTCAGCAA	60
tra.jav	TACCCTGAGGACAGATATCTTTCTGAGGAGCCACAGTCATCACCAACCTCTTATCAGCTA	60
trag.nap	TACCCTGAGGGCAAATATCTTTTGGAGGAGCTACAGTCATCACTAACCTTCTTTTCAGCAA	60
bala.acu	TACCCTGAGGACAAATATCATTTTGGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA	60
bala.bon	TACCCTGAGGACAAATATCATTTTGGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA	60
bala.bor	TACCCTGAGGACAAATATCATTTTGGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
bala.edi	TACCCTGAGGACAAATATCATTTTGGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
esch.rob	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA	60
bala.mus	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA	60
mega.nov	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTTCTATCAGCAA	60
bala.phy	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACTGTAATCACTAACCTCCTATCAGCAA	60
cap.mar	TGCCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA	60
ceph.com	TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA	60
ceph.eut	TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA	60
lage.obl	TACCCTGAGGACAGATATCATTCTGAGGCGCAACAGTCATCACCAACCTCCTATCAGCAA	60
ceph.heu	TACCCTGAGGACAAATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA	60
ceph.hec	TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA	60
lage.aus	TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA	60
lage.cru	TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA	60
lage.obs	TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA	60
lisso.bor	TACCCTGAGGACAGATATCATTTTGGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA	60
lisso.per	TACCCTGAGGACAGATATCATTTTGGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA	60
glo.mac	TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA	60
glo.mel	TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA	60
fere.att	TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA	60
pepo.ele	TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA	60
gram.gri	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA	60
pse.cra	TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTTCTATCAGCAA	60
lage.acu	TACCATGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAATCTCCTATCAGCAA	60
ordi.bre	TACCCTGAGGACAGATATCTTTCTGAGGCGCAACCGTCATCACTAATCTCCTATCAGCAA	60
orca.bre	TACCCTGAGGACAGATATCCTTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA	60
del.cap	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
del.tro	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
del.del	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.cly	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.coe	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
tur.adu	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.fro	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
saus.chi	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA	60
sten.lon	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA	60
turs.tru	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA	60
lage.alb	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACTAATCTCCTATCAGCAA	60
sten.bre	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAACCTCCTGTAGCAA	60
sota.flu	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAATCTCCTATCAGCAA	60



pero.pot	TCCCATGAGGACAAATATCATTCTGAGGTGCCACAGTAATCACAACCTCTCTATCAGCAA	60
gala.mat	TCCCATGAGGACAAATATCATTCTGAGGCGCTACCGTAATCACAATCTCTCTCTCAGCAA	60
gala.moh	TTCCGTGAGGACAAATATCATTCTGAGGCGCTACCGTAATCAGTAACCTCTCTCTCAGCAA	60
oto.gar	TCCCATGAGGACAAATGTCAATTCTGAGGCGCAACCGTAATTACAAATCTCTCTCTCAGCAA	60
lor.tar	TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACCAACCTACTATCAGCAA	60
nyc.cou	TCCCATGAGGACAAATATCATTCTGAGGTGCCACCGTCATCAGTAACCTACTATCAGCAA	50
mus	TTCCATGAGGACAAATATCATTCTGAGGTGCCACAGTTATTACAAACCTCTCTATCAGCAA	60
gorr	TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATCACAACCTTGCTATCAGCAA	60
homo	TCCCGTGAGGACAAATATCATTCTGAGGGGGCCACAGTAATTACAAACCTTACTATCAGCAA	60
dug.dug	TCCCATGAGGACAAATATCATTCTGAGGAGCAACCGTTATTACTAACCTCTCTCTCAGCTA	50
ele.max	TTCCATGAGGACAAATATCATTCTGAGGGGGCAACCGTAATTACTAACCTCTCTCTCAGCAA	50
afr.con	TCCCATGAGGACAAATATCATTCTGAGGGGGCAACTGTTCATCACAACCTTACTCAGCAA	60
pavo.mut	TCCCATGAGGTCAAATGTCAATTCTGAGGGGGCAACTGTTATCACAATCTATTCTCAGCAA	60
tra.bly	TCCCATGAGGACAAATATCATTCTGAGGGGGCTACCGTCATCACAACCTTATTCTCAGCAA	60
tra.sat	TCCCATGAGGACAAATATCATTCTGAGGGGGCTACCGTCATTACAAATTTATTCTCAGCAA	60
tra.cob	TCCCATGAGGACAAATATCATTCTGAGGGGGCTACCGTCATCACAATTTATTCTCAGCAA	60
tra.tem	TCCCATGAGGACAAATATCATTCTGAGGGGGCTACCGTCATCACAATTTATTCTCAGCAA	60
arg.arg	TCCCATGAGGACAAATATCATTCTGAGGGGGCTACCGTCATCACAACCTTATTCTCAGCAA	60
cat.wal	TTCCATGGGGACAAATATCATTCTGAGGGGGCTACTGTTCATCACAATCTATTCTCAGCAA	60
cro.cro	TCCCATGAGGACAAATATCATTCTGAGGGGGCTACCGTCATCACAATCTATTCTCAGCAA	60
sym.ree	TCCCATGAGGACAAATATCATTCTGAGGGGGCAACCGTCATCACAATTTATTCTCAGCAA	60
bam.tho	TCCCATGGGGACAAATATCATTCTGAGGGGGCTACCGTCATCACAATTTATTCTCAGCAA	60
fra.fra	TCCCATGAGGGACAAATATCATTCTGAGGGGGCTACCGTCATTACCAACCTACTCTCAGCAA	60
ith.cru	TACCATGAGGACAAATATCATTCTGAGGAGCCACTGTAAATCACAACCTACTCTCAGCAA	60
ant.par	TACCATGAGGACAAATGTCAATTCTGAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
ant.vir	TACCATGGGGACAAATGTCAATTCTGAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
gru.ant.ant	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATCACCATCTCTCTCAGCCG	60
gru.ant.gil	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATCACCATCTCTCTCAGCCG	60
gru.ant.sha	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATCACCATCTCTCTCAGCCG	60
gru.leu	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATCACCATCTCTCTCAGCCG	60
gru.can.pra	TGCCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACCAACCTCTCTCAGCCG	60
gru.can.row	TGCCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACCAACCTCTCTCAGCCG	60
gru.can.tab	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACCAACCTCTCTCAGCCG	60
gru.can.can	TACCATGGGGACAAATATCATTCTGAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
gru.ame	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
gru.gru	TACCATGGGGACAAATGTCAATTCTGAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
gru.mon	TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
gru.nig	TACCATGGGGACAAATATCATTCTGAGGGGGCTACAGTTATCACCATCTCTCTCAGCCG	60
gru.jap	TGCCATGAGGACAGATATCATTCTGAGGGGGCTACAGTCATCACCACCTATTCTCAGCTA	60
cic.boy	TACCATGAGGACAAATATCATTCTGAGGAGCCACTAGTTATTACCAACCTATTCTCAGCCA	60
zhe.ame	TACCATGAGGACAAATATCATTCTGAGGAGCCACTAGTTATTACCAACCTATTCTCAGCCA	60
ant.alb	TACCATGAGGGACAAATATCATTCTGAGGGGGCTACAGTTATCACCACCTATTCTCAGCAA	60
fal.fam	TACCCTGAGGACAAATATCATTCTGAGGGGGCTACAGTTATCACCACCTATTCTCAGCAA	60
fal.ver	TACCCTGAGGACAAATATCATTCTGAGGGGGCTACAGTTATCACCACCTATTCTCAGCAA	60
fal.per	TACCCTGAGGACAAATATCATTCTGAGGGGGCTACAGTTATCACCACCTATTCTCAGCAA	60
fal.spa	TACCCTGAGGACAAATGTCAATTCTGAGGAGCCACAGTCATTACCAACCTATTCTCAGCAA	60
ayt.ame	TACCATGAGGACAAATATCATTCTGAGGGGGCAACCGTGCATCACAACCTGTTCTCAGCTA	50
smi.sha	TCCCATGAGGGACAAATATCATTCTGAGGTGCTACAGTAATCACAACCTATTCTCAGCAA	60
vid.cha	TGCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATCACAACCTATTCTCAGCAA	60
chry.pic	TACCATGGGGACAAATATCATTCTGAGGTGCCACCGTTATTACTAACCTCTCTCAGCCA	60
emy.orb.kur	TACCATGAGGGACAAATATCATTCTGAGGTGCCACCGTTATTACTAACCTCTCTCAGCCG	60
che.mud	TACCATGAGGACAAATATCATTCTGAGGGGGCAACCGTGCATCACAACCTACTCTCAGCCA	60
eum.egr	TCCCATGGGGACAGATATCATTCTGAGGGGGCAACCGTAATTACCAACCTATTATCAGCAA	60
.....		
dep.mel	TCCCATACATTGGGTACAAACCTAGTAGAATGAATCTGAGGAGGCTTCTCAGTAGACAAAG	120
ore.ore	TTCCATATATTGGGCACAAACCTGGTAGAATGAATCTGAGGAGGCTTCTCTGGTAGACAAAG	120
adi.sas	TCCCATATATCGGCACAGATCTGGTAGAATGAATCTGAGGAGGCTTCTCTGGTAGACAAAG	120



ory.dam	TCCCATAACATCGGCACAAACCTAGTCGAATGAATTTGAGGGGGGATTCTCCGTAGACAAAG	120
hip.equ	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCCGTAGACAAAG	120
alc.bus	TCCCATATATTGGGCACAGACCTAGTAGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
sig.lic	TCCCATATATTGGGCACAGACCTAGTAGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
bea.hun	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
dam.lun	TTCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
con.tau	TCCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
amm.ler	TCCCATACATTGGGCACAGACCTGGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
pse.nay	TCCCCTATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
cap.ibe	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
hem.jem	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
cap.fal	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGATAAAG	120
rup.pyr	TCCCATACATTGGGCATAGACTTAGTCGAGTGAATCTGAGGGGGGCTTCTCCGTAGACAAAG	120
rup.rup	TCCCCTATATTGGGCACAGACTTAGTCGAATGAATCTGAGGGGGGCTTCTCCGTAGACAAAG	120
nem.cau	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
bud.tax.tax	TCCCATACATTGGGCACAAACCTAGTTGAGTGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
pan.hod	TCCCATACATTGGGCACAGACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
ovi.amm	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
ovi.vig	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
cap.cri	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCCGTAGACAAAG	120
ovi.mos	TCCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
ore.ame	TTCCATACATCGGTACAGACCTAGTCGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
cep.dor	TCCCATACATTGGGTACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGACAAAG	120
cep.max	TCCCATATATCGGCACAAACCTAGTTGAGTGAATCTGAGGGGGGCTTTTCAGTAGACAAAG	120
bis.bon	TCCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
bos.gru	TTCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
bos.tra	TCCCATACATCGGCACAAACCTAGTTGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
bub.min	TCCCATACATTGGGCACAAACCTAGTTGAGTGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
buba.bub	TCCCATACATTGGGTACAAACCTAGTTGAGTGAATCTGAGGGGGGCTTCTCCGTAGACAAAG	120
tra.ang	TCCCCTATATTGGGCACCAACCTAGTTGAATGAATCTGAGGGGGGCTTTTCAGTAGACAAAG	120
tra.eur	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAGG	120
kob.ell	TCCCATATATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
kob.meg	TCCCATATATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTCGATAAAG	120
red.aru	TCCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTCTCAGTCGATAAAG	120
red.ful	TCCCATACATCGGCACAAACCTAGTTGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
neo.mos	TCCCATATATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGACAAAG	120
pel.cap	TCCCATACATTGGGTACAAACCTAGTCGAATGAATCTGAGGGGGGATTCTCAGTAGATAAGG	120
gas.dam	TCCCATACATCGGCACAGACCTAGTAGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
our.our	TTCCATACATTGGGTACAAACCTAGTCGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
ant.cer	TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGGGGGCTTCTCAGTAGATAAAG	120
sai.tac	TCCCATATATCGGCACAGACCTAGTAGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
mad.kir	TCCCATATATCGGCACAAACCTAGTTGAATGAATCTGAGGGGGGCTTCTCAGTAGACAAAG	120
rap.mel	TTCCCTACATTGGGCACAAACCTAGTAGAATGAATCTGAGGGGGGATTCTCAGTTGATAAAG	120
gas.gas	TCCCATACATCGGCACAAACCTAGTAGAATGAATCTGAGGGGGGATTCTCAGTAGACAAAG	120
ant.ame	TCCCATACATTGGGTACTAACCTAGTAGAATGAATCTGAGGGGGGATTCTCAGTAGATAAAG	120
hyd.ine	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTTGATAAAG	120
mun.mun	TTCCATACATTGGGTACTAATCTAGTTGAATGAATTTGAGGGGGCTTTTCAGTAGACAAAG	120
alc.alc	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.ela.kan	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.ela.kan	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.ela.gin	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.nip.cen	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.nip.yes	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.nip.kes	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.nip.pul	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.nip.nip	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120
cer.ela.gin	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGGCTTTTCAGTAGACAAAG	120
cer.dam	TTCCATACATTGGGTACAAACCTAGTTGAGTGAATCTGAGGGGGGCTTTTCAGTAGATAAAG	120

ran.car	TTCCATATATTGGTACAAATCTAGTCCAATGAATTTGAGGAGGATTTTCTGTAGATAAAG	120
mos.fus	TTCCATACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTCTCAGTAGACAAAG	120
mos.leu	TTCCATACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTCTCAGTAGACAAAG	120
mos.chr	TTCCATACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTCTCAGTAGACAAAG	120
mos.ber	TTCCCTTACATTGGTACTAATCTGGTTGAATGAATCTGAGGAGGCTTCTCAGTAGACAAAG	120
mos.mos	TTCCCTTACATTGGTACTAATCTGGTTGAATGAATCTGAGGAGGCTTCTCAGTAGACAAAG	120
tra.jav	TCCCATAACATTGGGACAGACTTGGTCCAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
trag.nap	TCCCCTATATCGGCACCGAAGTAGTTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala.acu	TCCCATAATATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala.bon	TCCCATAACATTGGTACCACCTTAGTCCAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala.bor	TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGCTTCTCAGTAGATAAAG	120
bala.edi	TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGCTTCTCAGTAGATAAAG	120
esch.rob	TCCCATAACATTGGGACTACCTTAGTCCAATGGGCTGAGGCGGCTTCTCAGTAGATAAAG	120
bala.mus	TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGCTTCTCAGTAGATAAAG	120
mega.nov	TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala.phy	TCCCATAACATTGGTACCACCTTAGTCCAATGAATCTGAGGCGGCTTCTCAGTAGATAAAG	120
cap.mar	TCCCATAATATTGGTACCACCTTAGTCCAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
ceph.com	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph.eut	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.obl	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph.heu	TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGAGGATTTTCCGTAGACAAAG	120
ceph.hec	TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGAGGATTTTCCGTAGATAAAG	120
lage.aus	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.cru	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.obs	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lisso.bor	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lisso.per	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
glo.mae	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
glo.mel	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
fere.att	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
pepo.ele	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
gram.gri	TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
pse.cra	TCCCCTACATCGGTACCACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.acu	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
orci.bre	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
orca.bre	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
del.cap	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
del.tro	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
del.del	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
sten.cly	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
sten.coe	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
tur.adu	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
sten.fro	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
saus.chi	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
sten.lon	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
turs.tru	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
lage.alb	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
sten.bre	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
sota.flu	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
del.leu	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
mono.mon	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGATAAAG	120
plat.gan	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGATAAAG	120
plat.min	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGATAAAG	120
kogi.bre	TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGTGGAATTTTCCGTAGACAAAG	120
kogi.slm	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
phys.cat	TCCCCTATATTGGCACTACCTTAGTAGAATGAATCTGAGGTGGAATTTTCCGTAGATAAAG	120
lipo.vak	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
phoc.sla	TCCCCTACATCGGCACCACTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120

bera.bai	TTCCCTTATATCGGCCACTACTCTTGTGCGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG	120
ziph.car	TCCCTTATATCGGCCACTACTCTAGTTCGAATGAATCTGAGGTGGTTTTTTCAGTAGATAAAAG	120
meso.eur	TCCCTTATATTTGGCACTACTCTAGTTCGAATGAATCTGAGGTGGCTTTTCCGTAGATAAAAG	120
meso.bid	TTCCCTACATCGGCCACTACCCTAGTTGAATGAATCTGAGGTGGCTTTTCCGTAGACAAAAG	120
meso.den	TTCCCTTATATTTGGCACCACCCTAGTTCGAGTGAATCTGAGGTGGTTTTTCCGTAGACAAAAG	120
hype.amp	TTCCCTTATATCGGCCACTACCCTAGTTGAATGAATCTGAGGTGGTTTTTCTCCGTAGACAAAAG	120
meso.per	TCCCTTATATTTGGCACCACCCTAGTTGAATGAATTTTGAGGTGGCTTCTCCGTAGATAAAAG	120
pont.bla	TCCCTTACATCGGAACTACCCTTGTAGAAATGGATCTGAGGTGGTTTTCTCTGTAGACAAAAG	120
hex.lib	TCCCTTACATTGGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTTCTGTAGATAAAAG	120
hipp.amp	TCCCTTATATTTGGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTTCCGTAGACAAAAG	120
dic.sum	TCCCTACATCGGCCACCAGACCTTGTAGAAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG	120
rhin.son	TCCCTTATATCGGTACCAACCTTGTAGAGTGAATCTGAGGAGGATTCTCAGTCGACAAAAG	120
cera	TCCCTTACATCGGCCACCAACCTCGTAGAATGAATCTGAGGAGGATTCTCCGTGACAAAAG	120
equu	TCCCTTACATCGGTACTACGCTCGTAGAATGAATCTGAGGTGGATTCTCAGTAGACAAAAG	120
baby.bab	TTCCCTTATATCGGAAACGGACCTCGTAGAATGGATCTGAGGAGGCTTCTCCGTGACAAAAG	120
phac.afr	TCCCTTACATTGGGAACCAATCTGTAGAAATGAATCTGAGGAGGTTTTCTCCGTGACAAAAG	120
sus.bar	TCCCTTATATCGGAAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTTCCGTGACAAAAG	120
lus.scr.ewb3	TCCCTTATATCGGAAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTTCCGTGACAAAAG	120
lama.gla	TTCCATATGTTGGCACAACACTAGTTCGAATGAATTTGAGGAGGATTCTCCGTAGACAAAAG	120
lama.gua	TTCCATATGTTGGCACAACACTAGTTCGAATGAATTTGAGGGGGGTTTCTCCGTAGATAAAAG	120
vic.vic	TTCCATACGTTGGTACACACTAGTTCGAGTGGATTGAGGAGGATTCTCCGTAGATAAAAG	120
cam.bac	TTCCCTTATATCGGCCACAACACTAGTAGAATGAATTTGAGGTGGCTTCTCCGTAGACAAAAG	120
arc.for	TCCCTTACATTGGGACCAACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAAG	120
arc.gaz	TCCCTTACATCGGAACTAACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAAG	120
eum.jub	TCCCTTACATCGGAAACCAACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTCGACAAAAG	120
sal.cal	TCCCTTACATCGGAAACCAACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTCGACAAAAG	120
odo.ros	TTCCCTATGTAGGGAGTGAATCTGGTTCGAATGAGTCTGAGGGGGGTTTTTCTCAGTTGATAAAAG	120
pho.fasciata	TTCCCTATATCGGAAACCGACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAAG	120
pho.gro	TCCCTTACATCGGAAACCGATCTAGTAGAATGAATCTGAGGAGGTTTTCTCAGTTGATAAAAG	120
pho.vit	TCCCTTATGTTCGGAACCGACCTTGTAGAATGAATCTGAGGAGGTTTTTCTCAGTAGATAAAAG	120
cys.cri	TCCCTTACATCGGAGCCGATCTAGTAGAATGAATCTGAGGGGGATTCTCAGTCGATAAAAG	120
hyd.lep	TTCCCTTACATCGGAAACCGACCTAGTAGAATGAATTTGAGGCGGATTCTCAGTCGACAAAAG	120
lep.wed	TTCCCTTACATCGGAACTGACTTAGTAGAATGAATCTGAGGCGGATTCTCAGTTGACAAAAG	120
mir.leo	TCCCTTATGTTCGGAGACCGACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGACAAAAG	120
eri.bar	TCCCTTACATCGGGAGTGAATCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGACAAAAG	120
mon.sch	TCCCTTACATCGGAAACCGATCTAGTAGAATGAATCTGAGGAGGTTTTCTCAGTAGATAAAAG	120
hela.mal	TCCCTTATATTTGGAAACCGACCTAGTAGAATGAATCTGAGGGGGCTTTTCTGTAGATAAAAG	120
sel.thi	TCCCTTATATTTGGAAACAGACCTAGTAGAATGAATCTGAGGGGGCTTTTCTGTAGATAAAAG	120
ail.ful	TTCCCTATATTTGGAACTAACCTTGTAGAGTGAATCTGAGGAGGTTTTCTCAGTCGACAAAAG	120
fel	TTCCATACATCGGGACTGAACCTAGTAGAATGAATCTGAGGGGGCTTTCTCAGTAGACAAAAG	120
can	TCCCTTATATCGGAACTGACTTAGTAGAATGGATCTGAGGCGGCTTCTCAGTCGACAAAAG	120
tal	TTCCCTTACATCGGTACAGACTTAGTAGAATGAATTTGAGGTGGCTTCTCAGTAGACAAAAG	120
gla.sab	TTCCCTTATATTTGGGACAACACTTGTAGAATGAATCTGAGGAGGCTTCTCTGTGACAAAAG	120
gla.vol	TTCCCTTATATTTGGTACAACACTTGTAGAATGAATCTGAGGGGGCTTCTCTGTGATAAAAG	120
hyl.pha	TCCCTTACATTGGGAACAGTCCTTGTGGAATGAATTTGAGGGGGATTCTTCCGTAGATAAGG	120
pet.pez	TCCCTTATATTTGGAAACAGTCCTTGTGGAATGAATTTGAGGGGGATTCTTCCGTAGATAAGG	120
bel.pez	TCCCTTATATTTGGAACTGATCTAGTAGAGTGAATCTGAGGGGGCTTTTCTCAGTTGACAAAAG	120
pte.mom	TCCCTTATATCGGGACCAACCTTGTGGAATGGATCTGAGGTGGTTTTCTCAGTTGATAAAAG	120
gala.demi	TCCCATATATACGGCCCTACTCTAGTAGAATGAATCTGAGGGGGCTTTTCCGTAGACAAAAG	120
pero.pez	TCCCATATGTAGGTAGAACCCCTGTAGAATGAATTTGAGGGGGATTCTCAGTAGACAAAAG	120
gala.mat	TTCCCTTACATCGGTACCGCCCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG	120
gala.moh	TTCCCTTATATAGGAACCTGACTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG	120
oto.gar	TTCCCTTACATCGGAACTAACCTAGTTGAATGAATCTGAGGGGGATTCTCAGTAGATAAAAG	120
lps.car	TTCCCTTATATTTGGCACAACCTAGTTGAATGAATTTGAGGGGGATTCTCAGTAGATAAAAG	120
lys.cou	TCCCTTATATTTGGCACAACCTAGTTGAATGAATTTGAGGGGGATTCTCAGTAGATAAAAG	120
mus	TCCCTTATATTTGGAAACCAACCTAGTTGAATGAATTTGAGGGGGATTCTCAGTAGATAAGG	120
gatt	TCCCTTACATCGGAAACAGACCTAGTTGAATGAATTTGAGGGGGATTCTCAGTAGATAAGG	120
homo	TCCCTTACATTGGGACAGACCTAGTTGAATGAATTTGAGGGGGATTCTCAGTAGATAAGG	120

dug.dug	TCCCCTACATCGGGACCAACCTAGTCGAATGAGTTTGAGGGGGGATTCTCAGTAGACAAAG	120
ele.max	TTCCCCTACATCGGGACCAACCTAGTAGAATGAAATTTGAGGAGGGCTTTTCGGTAGATAAAG	120
afr.con	TCCCCTATATTGGTCAAACCTAGTAGAATGGGCTTGAGGAGGATTCTCAGTTGACAAAC	120
pavo.mut	TCCCCTTATATTGGACAAACCTAGTAGAATGAGCCTTGAGGGGGGATTCTCAGTCGACAAAC	120
tra.bly	TCCCATACATTTGGCCAAACCTTAGTAGAATGAGCCTTGAGGAGGGCTTTTCAGTTGACAAATC	120
tra.sat	TCCCATACATTTGGTCAAACCTTAGTAGAATGAGCCTTGAGGCCGGCTTTTCAGTTGACAAATC	120
tra.cob	TCCCATACATTTGGCCAAACCTTAGTAGAATGGGGCTTGAGGGGGGCTTTTCAGTTGACAAATC	120
tra.tem	TCCCATACATTTGGCCAAACCTTAGTAGAATGAGCCTTGAGGGGGGCTTTTCAGTTGACAAATC	120
arg.arg	TCCCCTATATTGGACAAACCTAGTAGAGTGAGCCTTGAGGAGGATTCTCAGTCGACAAAC	120
cat.wal	TCCCCTACATCGGACAGACCTTAGTAGAATGAGCCTTGAGGAGGATTCTCAGTTGACAAATC	120
cro.cro	TCCCCTACATTTGGACAAACCTAGTCGAGTGAGCTTGAGGGGGGCTTTTCAGTTGACAAAC	120
sym.ree	TCCCCTACATCGGACAAACCTAGTAGAGTGAGCTTGAGGGGGGATTCTCAGTAGACAAAC	120
bam.tho	TTCCCCTACATCGGACAAACCTAGTAGAATGAGCCTTGAGGGGGGATTCTCAGTAGACAAAC	120
fra.fra	TTCCCCTACATTTGGCCAAACCTTAGTAGAGTGAGCCTTGAGGGGGGATTCTCAGTAGATAAC	120
ith.cru	TTCCCCTACATCGGGCCAAACCTCTGTTAGAATGAGCTTGAGGAGGATTCTCAGTAGACAAAC	120
ant.par	TCCCATATATCGGGCCAAACCTTGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGACAAATC	120
ant.vir	TCCCATACATCGGGCCAAACCTTGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGATAATC	120
gru.ant.ant	TCCCCTACATCGGGCCAAACCTTGTAGAATGAGCTTGAGGGGGGCTTTCTCAGTAGACAAATC	120
gru.ant.gil	TCCCCTACATCGGGCCAAACCTTGTAGAATGAGCTTGAGGGGGGCTTTCTCAGTAGACAAATC	120
gru.ant.sha	TCCCCTACGGGGCCAAACCTTGTAGAATGAGCTTGAGGGGGGCTTTCTCAGTAGACAAATC	120
gru.leu	TCCCCTACATCGGGCCAAACCTTGTAGAATGAGCTTGAGGGGGGCTTTCTCAGTAGACAAATC	120
gru.can.pra	TCCCATACATCGGGCCAAACCTCGTAGAATGGGCTTGAGGGGGGCTTTCTCAGTAGACAAATC	120
gru.can.row	TCCCATACATCGGGCCAAACCTCGTAGAATGGGCTTGAGGGGGGCTTTCTCAGTAGACAAATC	120
gru.can.tab	TCCCATACATCGGGCCAAACCTCGTAGAATGGGCTTGAGGGGGGCTTTCTCAGTAGACAAATC	120
gru.can.can	TCCCATACATCGGGCCAAACCTCGTAGAATGGGCTTGAGGGGGGCTTTCTCAGTAGACAAATC	120
gru.ame	TCCCATACATCGGGCCAAACCTCGTAGAATGAGCTTGAGGGGGGCTTTCTCTGTAGACAAAC	120
gru.gru	TCCCATACATCGGGCCAAACCTCGTAGAATGAGCTTGAGGGGGGCTTTCTCAGTAGACAAAC	120
gru.mon	TCCCATACATCGGGCCAAACCTCGTAGAATGAGCTTGAGGAGGCTTTCTCAGTAGACAAAC	120
gru.nig	TCCCATACATCGGGCCAAACCTCGTAGAATGAGCTTGAGGAGGCTTTCTCAGTAGACAAAC	120
gru.jap	TCCCATACATCGGGCCAAACCTCGTAGAATGAGCTTGAGGGGGGCTTTCTCAGTAGACAAAC	120
cic.boi	TCCCCTACATCGGGCCAAACCTCGTAGAATGGGCTTGAGGGGGGCTTTCTCGGTGATAAAC	120
rhe.ame	TCCCCTACATCGGACAAACCTTGGTAGAATGAGCTTGAGGGGGGCTTTCTCAGTAGACAAAC	120
ant.alb	TCCCATACATCGGGCCAAACCTTAGTAGAATGGGCTTGAGGGGGGATTCTCTGTTGACAAAC	120
fal.fam	TCCCATACATCGGTCAAACCTAGTCGAGTCGGGCTTGAGGAGGATTCTCAGTAGACAAATC	120
fal.ver	TCCCATACATCGGGCCAAACCTAGTCGAATGGGCTTGAGGAGGATTCTCAGTAGATAAAC	120
fal.per	TCCCATACATCGGGCCAAACCTAGTCGAATGAGCTTGAGGGGGGATTCTCAGTAGACAAAC	120
fal.spa	TCCCATATATCGGGCCAAACCTAGTCGAATGGGCTTGAGGAGGATTCTCAGTAGACAAAC	120
ayc.ame	TCCCATACATCGGGCCAAACCTTGTAGAATGGGCTTGAGGAGGATTCTCTGTTGACAAAC	120
smi.sha	TTCCATACATCGGACAAACCTAGTAGAATGAGCTTGAGGAGGATTCTCAGTAGACAAAC	120
vid.cha	TTCCATACATTTGGCCAAACCTAGTAGAATGAGCCTTGAGGAGGATTCTCAGTAGACAAAC	120
chry.pic	TCCCATTTCATTGGTAAACACATTAGTACAAATGAATCTGAGGTGGAATCTCAGTAGACAAAC	120
emy.orb.kur	TCCCATACATTTGGCAATACACTAGTGAATGAATCTGAGGGGGATTCTCAGTAGATAAAC	120
che.mud	TCCCATACATCGGGCAACACACTAGTGAATGAATCTGAGGGGGATTCTCAGTAGACAAATC	120
eum.egr	TTCCATACATTTGGCCAAACCTAGTAGAATGAATTTGAGGGGGCTTTCTCGTAGACAAAC	120
	.. .. .	
sep.mel	CAACCCCTNACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
ore.ore	CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
add.nas	CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
ory.dam	CAACCCCTCACCAGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
hip.equ	CAACCCCTCACCAGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
alo.bus	CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
sig.lis	CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
bea.hun	CAACCCCTCACCAGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
dum.lun	CAACCCCTCACCAGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
con.hun	CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
amm.les	CTACTCTCACCAGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130
pus.nay	CTACTCTCACCAGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTCATTCGCGGACTAG	130

cap.ibe	CCACTCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTTACAGCCCTCG	130
hem.jem	CTACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTTGCAGCCCTCG	130
cap.fal	CCACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTTGCAGCCCTCG	130
rup.pyr	CTACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTTGCAGCCCTAG	130
rup.rup	CTACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTTGCAGCCCTAG	130
nem.cau	CTACTCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTTACAGCTACTG	130
bud.tak.tak	CATCCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGACCTCG	130
pan.hod	CTACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTCG	130
ovi.amm	CCACCCTGACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTCG	130
ovi.vig	CTACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTCG	130
cap.cri	CCACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTCG	130
ovi.mos	CCACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTCG	130
ore.ame	CTACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTCG	130
cep.dor	CAACTCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTCG	130
cep.max	CAACCCTCACT	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
bis.bon	CAACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
bos.gru	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
bos.tra	CAACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
bub.min	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
buba.bub	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
tra.ang	CAACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
tra.eur	CAACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
kob.ell	CAACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
kob.meg	CAACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
red.aru	CAACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
red.ful	CAACCCTCACT	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
neo.mos	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
pel.cap	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
gas.dam	CAACTCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
our.our	CAACTCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
ant.cer	CAACCCTTAAC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
sai.tat	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
mad.kir	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
rap.mel	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
gaz.gaz	CAACACTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
ant.ame	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
hyd.ine	CTACCCTGACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
mun.mun	CAACCCTCACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
alc.alc	CAACTCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.ela.kan	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.ela.xan	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.ela.can	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.nip.cen	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.nip.yes	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.nip.ker	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.nip.pul	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.nip.nip	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.ela.ste	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
cer.dam	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
san.sar	CAACCCTAACC	CGATTCTT	CGCCTT	CCACTT	CGCTCCCA	TTTCATCATTCOCAGCCCTTG	130
mos.fus	CAACACTCA	CTCGATT					

[illegible]

hipp.amp	CCACCCTTACACGATTCTTTGGCTTCCACTTTATTCTTCCATTTCOTTATCACAGCACTAG	120
dic.sum	CCACCCTCACCCTGTTCTTTGGCTTCCACTTTATCTCTCCCTTCATCATCTAGCCCTAG	130
rhin.son	CTACCCTTACCCGATTCTTTGGCTTCCACTTTATCTCTCCCTTTATTATTCATAGCCCTAG	130
cera	CCACACTTACACGATTCTTTGGCTTCCACTTTATCTCTCCCTTTATTATTCATAGCCCTAG	130
equu	CCACCCTTACCCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCACAGCCCTGG	130
baby.bab	CAACCCTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCACAGCCCTGG	130
phac.afr	CAACTCTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
sus.bar	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
sus.ser.ewb3	CAACCCTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
lama.gla	CCACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
lama.gua	CCACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
vic.vic	CCACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
cam.bac	CCACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
arc.for	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
arc.gaz	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
eum.jub	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
zal.cal	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
odo.ros	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
pho.fasciata	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
pho.gro	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
pho.vit	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
cys.cri	CAACTCTAACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
hyd.lep	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
lep.wed	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
mir.leo	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
eri.bar	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
mon.sch	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
hela.mal	CGACTCTAACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
sel.chi	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
ail.ful	CAACTCTAACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
fel	CCACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
can	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
tal	CGACACTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
gla.sab	CTACCCTTACCCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
gla.vol	CTACCCTTACCCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
hyl.pha	CTACCCTTACCCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
pet.set	CTACCCTTACCCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
bel.pea	CAACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
pte.mom	CTACCCTTACCCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
gala.demi	CTACCCTTACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
pero.pot	CCACCCTTACTCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
gala.mat	CTACTCTTACCCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
gala.moh	CAACCCTCACCCTGTTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
oto.gar	CAACCCTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
lor.tar	CCACACTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
nyd.cou	CCACACTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
mus	CTACCCTTACCCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
gort	CCACCCTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
homo	CCACCCTCACACGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
dug.dug	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
ele.mak	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
afr.con	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
pavo.mut	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
tea.bly	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
tea.sit	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
tea.tob	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
tea.tem	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130
tea.tog	CAACCCTTAAACCGATTCTTTGGCTTCCACTTTATTCTACCTTTATCATCGCTGCCCTAG	130

cat.wal	CAACTCTCACCCGATTCTTCGCCCTTGCACCTTCCTCTCCCTTCGTAATTGCAGGAATCA	130
cro.cro	CAACCCCTCACCCGATTCTTCGCCCTTACACTTCCTCTCCCTTCGTAATTGCAGGAATTA	130
sym.ree	CAACCCCTCACCCGATTCTTCGCCCTTACACTTCCTCTACCCTTCGTAATTCACAGGAATCA	130
bam.tho	CAACTCTCACCCGATTCTTCGCCCTTACACTTCCTACTCCCTTCGTAATTCGAGGAATTA	130
fra.fra	CAACCCCTCACCCGATTCTTCGCCCTTACACTTCCTTCTGCCCTTCGTAATTGCAGGAATCA	130
ich.cru	CAACCCCTCACCCGATTCTTCGCCCTTACACTTTCTCTCCCTTCGCAATTCGAGGAATTA	130
anc.par	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTTCGATTGCATAATTATAGGGCTCA	130
anc.vir	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTTCGATTGCATAATTATAGGGCTCA	130
gru.anc.anc	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTTCGATTGCATAATTCATAGGGCTCA	130
gru.anc.gil	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTTCGATTGCATAATTCATAGGGCTCA	130
gru.anc.sha	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTTCGATTGCATAATTCATAGGGCTCA	130
gru.leu	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTTCGATTGCATAATTCATAGGGCTCA	130
gru.can.pra	CCACATTAAACCCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTATAGGGCTCA	130
gru.can.row	CCACATTAAACCCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTATAGGGCTCA	130
gru.can.tab	CCACATTAAACCCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTATAGGGCTCA	130
gru.can.can	CCACATTAAACCCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTCATAGGGCTCA	130
gru.ame	CCACATTAAACCCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTCATAGGGCTCA	130
gru.gru	CCACATTAAACCCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTCATAGGGCTCA	130
gru.mon	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTCATAGGGCTCA	130
gru.nig	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTCATAGGGCTCA	130
gru.jap	CCACATTAACTCGATTCTTCACCTTTACACTTCCTCTCCGATTGCATAATTCATAGGGCTCA	130
cic.boy	CAACACTAACCCGATTCTTCGCCCTTACACTTTCTTCTGCCCTTCGCAATTCGAGGGCTCA	130
rhe.ame	CTACCCCTAACCCGATTCTTCGCCCTTGCACCTTCCTTCTGCCCTTCGTAATTCGAGGCATTA	130
anc.alb	CAACCCCTGACACGATTCTTCGCCCTTACACTTTCTCTGCCCTTCGTAATTCGAGGCCTAG	130
fal.fam	CAACACTGACCCGATTCTTCGCCCTTACACTTCCTCTACCATTCCTAATTCGAGGGCTCA	130
fal.ver	CAACACTAACCCGATTCTTCGCCCTTACACTTTCTCTACCATTCCTAATTCGAGGGCTCA	130
fal.per	CAACACTGACCCGATTCTTCGCCCTTACACTTCCTACTTCCATTCCCTAATTCGAGGGCTTA	130
fal.spa	CAACACTAACCCGCTTCTTCGCCCTTACACTTCCTACTTCCATTCCCTAATTCGAGGGCTTA	130
ayt.ame	CAACCCCTAACTCGATTCTTCGCCCTTACACTTCCTACTACCCCTTCCTAATTCGAGGAATCA	130
smi.sha	CCACCCCTTACCCGATTCTTCGCCCTTACACTTCCTCTCCCATTTATCATTCGCAAGCCTGA	130
vid.cha	CAACACTCACCCGATTCTTCGCCCTTACACTTCCTTCTACCCCTTCCTCATTCGAGGACTCA	130
chry.pic	CAACCTTAACCCGATTCTTTACCCCTTACACTTCCTTCTACCATTTACAAATTCATAGGTCTAA	130
emy.orb.kur	CAACCCCTAACCCGATTCTTCACCTTTCCCATTTCTTACTGCCATTTACCATTTATAGGGCTAA	130
che.mud	CAACCCCTAACCCGATTCTTCACCTTCCACTTCCTAATAGCAATTCGCCATTACCGGCCCTTA	130
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aap.mel	CCATAGTCCACCTACTCTTTTCTCCACGAAACAGGATTTAAACAACCCCTACAGGAATCTTAT	240
ore.ore	CCATAGTACACCTACTCTTTTCTCCACGAAACAGGCTTCAATAACCCCCACAGGAATCTCAT	240
add.nas	CCATAGTCCATCTACTCTTTTCTCCACGAAACAGGCTTCAACAACCCCTACAGGAATCTCCT	240
ory.dam	CCATAGTCCACCTACTCTTTTCTCCACGAAACAGGCTTCAACAACCCCTACAGGAATTCACCT	240
hig.equ	CCATAGTACACCTACTCTTTTCTCCATGAGACAGGCTTCAACAACCCCCACAGGAATTTGAT	240
alc.bus	CCATAGTTCACCTCTTATTCTCTCCACGAAACAGGATTTAAACAACCCCCACAGGAATCTCAT	240
sig.lic	CCATAGTTCACCTCTTATTCTCTCCACGAAACAGGATTTAAACAACCCCCACAGGAATCTCCT	240
bea.hun	CCATAGTCCACCTCTTATTCTCTCCACGAAACAGGATTTAAACAACCCCCACAGGAATCTCCT	240
dam.lun	CCATAGTGCACCTCTTATTCTCTCCATGAAACAGGATTTAAACAACCCCCACAGGAATCTCAT	240
con.tau	CTATAGTCCATCTCTTATTCTCTCCACGAAACAGGATTTAAACAATTTCCACAGGAATTTGAT	240
amm.les	CCATAGTCCACCTACTCTTTTCTCTCATGAAACAGGATTTCAACAACCCCCACAGGAATTTGAT	240
pse.nay	CCATAGTCCACCTACTCTTTTCTCTCCACGAAACAGGATTTAAACAACCCCCACAGGAATTTGAT	240
cap.ibe	CCATAGTCCACCTCTCTCTCTCTCCACGAAACAGGATTTCAACAACCCCCACAGGAATTTGAT	240
hem.jem	CCATAGTCCACCTCTCTCTCTCTCCACGAAACAGGATTTCAACAACCCCCACAGGAATTTGAT	240
cap.fal	CCATAGTCCACCTACTCTTTTCTCTCCATGAAACAGGATTTCAACAATTTCCACAGGAATTTGAT	240
sup.pyt	CCATAGTCCACCTACTCTTTTCTCTCCATGAAACAGGATTTCAACAATTTCCACAGGAATTTGAT	240
sup.sup	CCATAGTCCACCTACTCTTTTCTCTCCATGAAACAGGATTTCAACAATTTCCACAGGAATTTGAT	240
hem.cau	CCATAGTCCACCTACTCTTTTCTCTCCATGAAACAGGATTTCAACAATTTCCACAGGAATTTGAT	240
bud.bak.bak	CCATAGTCCACCTACTCTTTTCTCTCCATGAAACAGGATTTCAACAATTTCCACAGGAATTTGAT	240
gan.hod	CCATAGTCCACCTACTCTTTTCTCTCCATGAAACAGGATTTCAACAATTTCCACAGGAATTTGAT	240
avi.amm	CCATAGTCCACCTACTCTTTTCTCTCCATGAAACAGGATTTCAACAATTTCCACAGGAATTTGAT	240



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cap.cri	CCATAGTGCACCTACTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
ovi.mos	CTATAGTACATTTGCTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
ore.ame	CCATAGTCCACCTTACTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTCAT	240
cep.dor	CCATAGTTCACCTACTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cep.max	CCATAGTCCACCTACTTATTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTCAT	240
bis.bon	CCATAGTTCACCTACTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bos.gru	CCATAGTCCACCTACTTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bos.tra	CAATAATCCATCTACTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bub.min	CAATAGTCCACCTATTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
buba.bub	CAATAGTCCACCTATTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
tra.ang	TTATGGTCCACCTATTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
tra.eur	CCATGGTACACCTACTTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
kob.ell	CCATAGTCCATCTTCTGTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTCAT	240
kob.meg	CTATAGTTCACCTACTTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
red.aru	CTATAGTACACCTACTTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
red.ful	CTATAGTCCACCTACTTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
neo.mos	CCATAGTCCACCTACTTATTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
pel.cap	CCATAGTACACTTCTGTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
gaz.dam	CCATAGTTCATCTATTATTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
our.our	CCACAGTCCACCTACTTATTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
ant.cer	CCATAGTACACCTACTGTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
sai.tat	CTATAGTCCACCTACTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
mad.kir	CCATGGTTCACCTCTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
rap.mel	CTATAGTTCACCTACTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
gaz.gaz	CTATAGTCCACCTATTATTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
ant.ame	CCATAGTACACTTACTTATTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
hyd.ine	CCATAGTGCACCTACTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
mun.mun	CTATAGTCCACCTACTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
alc.alc	CCATAGTCCACCTACTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cer.ela.kan	CTATAGTACACTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cer.ela.xan	CTATAGTACACTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cer.ela.can	CTATAGTACACTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cer.nip.cent	CTATAGTACACTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cer.nip.yes	CTATAGTACACTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
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cer.nip.pul	CTATAGTACACTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cer.nip.nip	CTATAGTACACTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cer.ela.sco	CTATAGTACACTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cer.dam	CTATAGTACATTTACTTCTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
ran.tar	CTATAGTCCATTTGCTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
mos.fus	CTATGGTTCACCTACTCTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
mos.leu	CTATGGTTCACCTACTCTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
mos.chr	CTATGGTTCACCTACTCTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
mos.ber	CCATGGTTCATCTACTCTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
mos.mos	CCATGGTTCATCTACTCTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
tra.jav	TCCTAGTCCACCTTTTATTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
trag.nap	CCCTAGTCCACCTTTTATTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bala.atu	CAATTCTCCACCTGATTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bala.bon	CAATTCTCCACCTGATTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bala.ber	CAATTCTCCACCTGATTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bala.edi	CAATTCTCCACCTGATTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
esch.sco	CAATTCTCCACCTGATTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bala.mus	CAATTCTCCACCTGATTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
neg.mos	CAATTCTCCACCTGATTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
bala.phy	CAATTCTCCACCTGATTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
cip.mic	CAAGCTCTTCATCTCTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240
caph.rom	CAAGCTCTTCATCTCTTTTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCAT	240

ceph.eut CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
lage.obl CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
ceph.heal CAGCCGTCCATCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
ceph.hec CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
lage.aus CAGCCGTCCACTTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
lage.cru CAGCCGTCCACCTGCTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
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lisso.bor CAGCTGTTACCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
lisso.per CAGCTGTTACCTACTGTTCTACACGAGACAGGATCCAATAACCCCATAGGAATCCCAT 240  
glo.mac TAGCTGTCCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCATAGGAATCCCAT 240  
glo.mel TAGCTGTCCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCATAGGAATCCCAT 240  
fere.att TAGCTGTCCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCTACAGGAATCCCAT 240  
pepo.ele TAGCTGTTACCTGCTATTCTACACGAGACAGGATCCAATAACCCACAGGAATCCCAT 240  
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pse.cra CAGCTGTTACCTGCTGTTCTACACGAGACAGGATCCAATAACCCCTACAGGAATCCCAT 240  
lage.acu CAGCTGTTACCTACTGTTCTACACGAGACAGGATCCAATAACCCACAGGAATCCCAT 240  
orci.bre TAACTGTTACCTACTATTCTACACGAAACAGGATCCAACAATCCTACAGGAATCCCAT 240  
orca.bre CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCACAGGAATCCCAT 240  
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del.tro CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCACAGGAATCCCAT 240  
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sten.cly CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCACAGGAATCCCAT 240  
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sten.fro TAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCACAGGAATCCCAT 240  
saus.chi CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
sten.lon CAGCCGTCCACCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
turs.tru TAGCTGTTACCTACTATTTTACACGAGACAGGATCCAACAACCCACAGGAATCCCAT 240  
lage.alb CAACTGTCCACCTACTATTCTACACGAGACAGGATCCAACAATCCACAGGAATCCCAT 240  
sten.bre CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAATCCACAGGAATCCCAT 240  
sota.flu TAGCCGTCCATTATTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
del.leu TGGCCGTCCACTTATTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
mono.mon CAATTATCCACCTACTATTCTACACGAAACAGGCTCAAACAACCCACAGGAATCCCAT 240  
plat.gan CAGTTATCCACCTACTATTCTACACGAAACAGGCTCAAACAACCCCATAGGAATCCCAT 240  
plat.min CAATGGTCCACCTCTTATTCTCCACGAAACAGGATCCAACAACCCCATAGGAATCCCAT 240  
kogi.bre CAATAATCCACCTCTTATTCTCCACGAAACAGGATCCAACAACCCCTAGGAATTCCTT 240  
kogi.sim CAATAGTACATCTCTATTCTCCATGAAACAGGATCCAACAACCCACAGGAATTCCTT 240  
phys.cat CAACCGTCCACTTACTATTCTCCATGAAACAGGATCCAACAACCCATAGGAATTCCTT 240  
lipo.vex TAATCGTCCATCTACTATTCTCCATGAAACAGGCTCCAACAATCCACAGGAATCCCAT 240  
phoc.sin CAGCCGTCCACTTACTATTCTCCACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240  
bera.bai CAGCCGTCCACTTACTATTCTCCACGAAACAGGATCTAATAACCCACAGGAATCCCAT 240  
ziph.car CAATCGTCCACTTACTATTCTCCATGAAACAGGATCTAACAACCCCTACAGGAATTCCTT 240  
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meso.bid CAATCGTCCACCTACTATTCTCCATGAAACAGGATCCAACAATCCACAGGAATTCCTT 240  
meso.den CAATTGTCCATTACTATTCTACACGAAACAGGATCTAATAATCCCATAGGAATTCCTT 240  
hype.amp TTATAGTCCACCTGCTATTCTACACGAAACAGGATCCAACAACCCACAGGAATTCCTT 240  
meso.per CCGCCGTCCACCTACTGTTCTCCACGAAACAGGCTCCAACAACCCACAGGAATTCCTT 240  
pont.bla CCATCGTCCATCTACTATTCTCCATGAAACAGGATCCAACAACCCATCAGGAATTCCTT 240  
hex.lib CAATTAGCCACCTGCTATTCTACACGAAACAGGATCCAATAACCCATCAGGAATTCCTT 240  
hipp.amp CAGTCCACCTACTATTCTACACGAAACAGGATCCAATAACCCATCAGGAATTCCTT 240  
dic.sum CAATCACCACCTACTATTCTCCACGAAACAGGATCCAATAACCCATCAGGAATTCCTT 240  
chin.son TAACTGTCCATCTACTATTCTCCACGAAACAGGATCCAACAACCCCTACTGGAATTCCTT 240  
cera GAACCGTACATCTATTATTCTCCACGAAACAGGATCCAATAACCCCTACTGGAATTCCTT 240  
equu GAACCGTACATCTATTATTCTCCACGAAACAGGATCCAATAACCCCTACTGGAATTCCTT 240  
baby.bab GAACCGTACATCTATTATTCTCCACGAAACAGGATCCAATAACCCCTACTGGAATTCCTT 240  
phac.aff CAGCCGTACATCTCTATTCTTAACGAAACAGGATCCAATAACCCCTACTGGAATTCCTT 240  
sus.bar CAGCCGTACATCTCTATTCTTAACGAAACAGGATCCAATAACCCCTACTGGAATTCCTT 240  
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lama.gua	CAGGAGTGCATCTACTATTTTACACGAAACAGGGCTCCAACAATCCAACAGGAATTTCTT	240
vic.vic	CGGGAGTACATCTACTATTTTACACGAAACAGGGCTCCAACAATCCAACAGGAATTTCTT	240
cam.bac	TAGCCGTACACCTATTATTCCTACACGAAACAGGGCTCTAATAACCCCGACAGGAATCTCCT	240
arc.for	TAATAGTACATCTGCTATTTCCTACATGAAACAGGATCCAATAACCCCATCAGGAGTCTCCT	240
arc.gaz	TAATAGTGCACCTACTATTTCCTACACGAAACAGGATCCAACAACCCCATCAGGAGTCTCCT	240
eum.jub	TAATAGTACACCTATTATTCCTACACGAAACAGGATCCAACAATCCAATCAGGAATCTCCT	240
zal.cal	TAATAGTACACCTATTATTCCTACACGAAACAGGATCCAACAATCCAATCAGGAATCTCCT	240
odo.ros	CAGCAGTACACCTACTATTTCCTACACGAAACAGGATCCAACAACCCCTCCGGAATCGTAT	240
pho.fasciata	CGGCAGTTCACCTACTATTTCCTACACGAAACAGGATCCAACAACCCCATCAGGAATCGTAT	240
pho.gro	CGGCAGTTCACCTACTATTTCCTACACGAAACAGGATCCAACAACCCCATCAGGAATCGTAT	240
pho.vit	CAGCAGTCCACCTACTATTTCCTACACGAAACAGGATCCAACAACCCCTCCGGAATCATAT	240
cys.cri	CAACAGTCCACCTACTATTTCCTACACGAAACAGGATCTAATAATCCCTCCGGAATCACAT	240
hyd.lep	CAGCAGTACATCTACTATTTCCTACACGAAACAGGATCCAATAACCCCTCCGGAATCCCAT	240
lep.wed	CAGCAGTACATCTACTATTTCCTACACGAGACAGGATCCAACAACCCCTCCGGAATCCCAT	240
mir.leo	CAGCAGTACATCTACTATTTCCTACACGAAACAGGATCCAACAACCCCTCTGGAATCCCAT	240
eri.bar	CAGCAGTCCACCTATTATTCCTACACGAAACAGGATCCAACAACCCCTCCGGAATCTCGT	240
mon.sch	CAGCAGTCCACCTATTATTCCTACACGAAACAGGATCCAACAATCCCTCCGGAATCCCAT	240
hela.mal	CAGCGGTCCACCTATTATTCCTACACGAAACAGGGTCCAACAATCCCTCTGGAATCCCAT	240
sel.thi	CAGCAGTTCATCTATTGTTCTACACGAAACAGGATCCAACAACCCCTCTGGAATCCCAT	240
ail.ful	CAACTATCCATCTCTTATTCCTACATGAAACAGGATCTAATAACCCCTCAGGCATCCCAT	240
fel	CAGGAGTACACCTCTTATTCCTTCTACGAAACAGGATCTAACAACCCCTCAGGAATTACAT	240
can	TAATAGTACACCTCTTATTCCTTCTACACGAAACAGGATCCAACAACCCCTCAGGAATCACAT	240
tal	CTGGAGTTCACCTGTTATTTCTTACGAAACAGGATCAAACAACCCCATCAGGACTCTCAT	240
gla.sab	CCATAATCCATCTACTCTTTTACACGAAACAGGATCCAATAACCCCATCAGGACTAATCT	240
gla.vol	CCATAATCCATCTACTCTTTTACACGAAACAGGATCCAATAACCCCATCAGGACTAATCT	240
hyl.pha	CTATAATTACCTTCTCTTCTTACACGAAACAGGATCAAATAACCCCATCAGGCCTAATTT	240
pet.set	CTATAATCCACCTTCTCTTCTTACACGAAACAGGGTCAAATAATCCATCAGGTCTAATTT	240
bel.pea	CAATAGTCCACCTTCTTTTCTTCCACGAAATTTGGGTCAAATAATCCCTCCGGAATTAATTT	240
pte.mom	CAATAGTTCACCTACTTTTCTTCTTACGAAACAGGGTCCAACAACCCCATCTGGACTTACCT	240
gala.demi	TCATAATCCACCTCCTATTCTTCTTACGAAACAGGATCAAACAACCCCTCAGGACTTCCAT	240
pero.pot	CCACAACCTCACCTCTTATTTCTTACGAAACAGGATCAAATAACCCCATCAGGAATCTCAT	240
gala.mat	CCATAATTACCTTCTTTTCTTCTTACATGAAACAGGATCAAACAACCCCTCAGGAATCTCAT	240
gala.moh	CCATAATTACCTTCTTTTCTTCTTACATGAAACAGGGTCAAATAACCCCTCCGGAATCTCAT	240
oto.gar	TCATAATCCACCTCCTTTTCTTCTTCCACGAAATCAGGATCAAACAACCCCTCAGGAATCCCAT	240
lor.tar	CTGCAATTACCTACTTTTCTTCTTACACGAAATCAGGATCAAATAACCCCATCCGGAATTAACAT	240
nyc.cou	TTGTGATTACCTCATCTTTTCTTACATGAAACAGGGTCAAATAATCCATCAGGAATCTCAT	240
mus	CAATCGTTACCTCCTCTTCTTCTTCCACGAAACAGGATCAAACAACCCCTCAGGATTAACCT	240
gorr	CAACCCCTCCATCTCCTATTCTTCTTACACGAAACAGGATCAAACAACCCCTCAGGATTAACCT	240
homo	CAACACTCCACCTCCTATTCTTCTTCTTGCACGAAACAGGGATCAAACAACCCCTCAGGATTAACCT	240
dug.dug	TAATAGTCCACTTACTATTTCCTTCCACGAAACAGGGTCCAACAACCCCATCAGGACTGATCT	240
ele.max	CAGGAGTGCACCTAACCTTTCTTTCACGAAACAGGGTCAAACAACCCCATCAGGACTGATCT	240
afr.con	CAATTATCCACCTCACATTCCTTCTTCTTACATGAAATCAGGCTCAAACAACCCCATCAGGACTGATCT	240
pavo.mut	CAATTATCCACCTCACATTCCTTCTTCTTACATGAAATCAGGCTCAAATAATCCATCAGGACTGATCT	240
tra.bly	CCATCATGCCACCTCATCTTCTTCTTACATGAAATCAGGCTCTAATAACCCCATCAGGACTGATCT	240
tra.sas	CTATCATACACCTCATCTTCTTCTTACATGAAATCAGGCTCTAATAACCCCATCAGGACTGATCT	240
tra.cob	CCATCATCCACCTCATCTTCTTCTTACATGAAATCAGGCTCTAATAACCCCATCAGGACTGATCT	240
tra.tem	CCATCATCCACCTCATCTTCTTCTTACATGAAATCAGGCTCTAATAACCCCATCAGGACTGATCT	240
arg.arg	CCATCATCCACCTCACATTCCTTACACGAAATCAGGCTCAAACAACCCCATCAGGACTGATCT	240
cat.wal	CCATCATCCACCTCATCTTCTTCTTACATGAAATCAGGCTCAAATAACCCCATCAGGACTGATCT	240
cro.cro	CTGTCACCCACCTCATATTCTTCTTACACGAAATCAGGCTCAAACAACCCCATCAGGACTGATCT	240
sym.ree	CCATCATCACATCTTATTTCTTCTTACACGAAATCAGGCTCAAACAACCCCATCAGGACTGATCT	240
bam.cho	CCATTATCCACCTCACATTCCTTACACGAAATCAGGCTCAAACAACCCCATCAGGACTGATCT	240
fra.fra	CTATCATCCACCTCACATTCCTTCTTCTTACACGAAATCAGGCTCAAACAACCCCATCAGGACTGATCT	240
ith.cru	CTGTCACCCACCTCATATTCTTCTTACACGAAATCAGGCTCAAACAACCCCATCAGGACTGATCT	240
ant.par	CCCTAATCCACCTCATCTTCTTCTTCTTACAGGATCCGGCTCAAACAACCCCATCAGGACTGATCT	240
int.vic	CCCTAATCCACCTCATCTTCTTCTTCTTACAGGATCCGGCTCAAACAACCCCATCAGGACTGATCT	240
gou.ans	CCCTAATCCACCTCATCTTCTTCTTCTTACAGGATCCGGCTCAAACAACCCCATCAGGACTGATCT	240

gru.ant.gil	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATCGTAT	240
gru.ant.sha	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGTTCAAACAACCCCTAGGCATCGTAT	240
gru.leu	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATCGTAT	240
gru.can.pra	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATTGTAT	240
gru.can.row	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAATCCCTAGGCATTGTAT	240
gru.can.tab	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATTGTAT	240
gru.can.can	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATTGTAT	240
gru.ame	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATCGTAT	240
gru.gru	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATCGTAT	240
gru.mon	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATCGTAT	240
gru.nig	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATCGTAT	240
gru.jap	CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCTAGGCATCGTAT	240
cic.boy	CCCTAATCCACCTCACCTTCCTTCACGAGTCCGGCTCAAACAACCCCTAGGCATCATCT	240
rhe.ame	CTCTTATCCACCTCACCTTCCTTCACGAATCCGGTCCAACAACCCCTTAGGAATCGTAT	240
ant.alb	TCCTAATTCACCTGGCATTCCTTCACGAATCAGGCTCAAACAACCCCTAGGCATCACAT	240
fal.fam	CCCTAATCCACCTCACCTTCCTTCACGAATCAGGTTCAAACAACCCCTTAGGAATCACAT	240
fal.ver	CCCTAATTCACCTCACCTTCCTTCACGAATCAGGTTCAAACAACCCCTTAGGAATCACAT	240
fal.per	CCCTAATCCACCTCACCTTCCTTCACGAATCAGGTTCAAATAACCCCTTAGGAATCACAT	240
fal.spa	CCTTAATCCACCTCACCTTCCTTCACGAATCAGGTTCAAACAACCCCTTAGGAGTCACAT	240
ayt.ame	CCCTAGTCCACCTAATCTTCCTTCACGAGTCCGGCTCAAACAACCCCTAGGCATTGTAT	240
smi.sha	CACCTCATCCATCTCACCTTCCTTCACGAATCAGGTTCAAACAACCCCTTAGGTATCTCAT	240
vid.cha	CTCTAGTCCACCTCACATTTCCTTCACGAATCAGGATCAAACAATCCAATAGGAATTCCAT	240
chry.pic	CAATAGTACACCTACTTTTTCTTCACGAATCAGGATCAAACAACCCCAACAGGATTAACT	240
emy.orb.kur	CAATAGTACACCTACTCTTCTTCACGAATCAGGATCAAACAATCCAACAGGATTAACT	240
che.mud	CAGCAGTACATCTATTATCTTCACGAATCAGGATCAAACAACCCCAACAGGATTAACT	240
eum.egr	CAATAATTCACCTACTATTTCTTCACGAATCAGGATCAAATAACCCCAACGGACTAAAT	240
	* * * * *	
aep.mel	CAGATTTCAGATAAAAATTCGATTCACCCCTTACTATATACTATTRAAGACATCCTAGGAATCC	300
ore.ore	CAGACACAGACAAAATCCCATTTTCACCTTATTACACAATCAAAGATATCCTAGGCGCCC	300
add.nas	CAGACACAGACAAAATCCCATTTTCACCCCTTACTATACCATTAAAGACATCCTAGGCGCCC	300
ory.dam	CAGACACAGACAAAATCCGTTTCACCCCTTATTATACCATTAAAGATATCCTAGGCGCCC	300
hip.equ	CAGACTCCGATAAAAACCCCATTCACCCCTTACTACACCATTAAGACATTCTAGGCGCCC	300
alc.bus	CAGACCGAGATAAAAATCCCATTTTCACCCCTTACTATACAATCAAGGACATTCTAGGCGCCC	300
sig.lic	CAGACGCAGATAAAAATCCCATTTTCACCCCTTACTACACCATTAAGACATCCTAGGCGCCC	300
bea.hun	CAGATGCGAGATAAAAATCCCATTTTCACCCCTTACTACACTATCAAAGACGCCCCTAGGGGCCC	300
dam.lun	CAGATGCGGACAAAATCCCGTTTCACCCCTTACTACACTATCAAAGACGCCCCTAGGGGCCC	300
con.tau	CCGACACCGATAAAAATCCCATTTTCACCCCTTATTACACCATTAAGACATCCTAGGCGCTC	300
amm.ler	CAGACGCAGACAAAATCCCATTTTCACCCCTTACTACACCATTAAGATATTCTAGGCGCTG	300
pse.nay	CAGACACAGACAAAATCCCATTTTCACCCCTTACTACACCATTAAGATATTCTAGGCGCTG	300
cap.ibe	CAGACACAGACAAAATCCCATTTTCACCCCTTACTACACCATTAAGATATTCTAGGCGCTG	300
hem.jem	CAGATACAGACAAAATCCCATTTTCACCCCTTACTACACCATTAAGATATTCTAGGCGCTG	300
cap.fal	CAGACACAGACAAAATCCCATTTTCACCCCTTACTACACCATTAAGATATTCTAGGCGCTG	300
rup.pyr	CAGATGCGGATRAAAAATCCCATTTTCACCCCTTACTATACCATTAAAGACATTCTAGGCGCTG	300
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nem.cau	CAGACATAGACAAAATCCCATTTTCACCCCTTATTATACAATCAAAGATATTCTAGGCGCTA	300
bud.tax.tax	CAGATGCGAGATAAAAATTCGATTTTCACCCCTTATTACACCATTAAGATATCCTAGGAGTCA	300
pan.hod	CAGATGCGAGACAAAATTCGATTTTCACCCCTTACTATACCATTAAAGACATCCTAGGCGCTA	300
ovi.amm	CGGACACAGATAAAAATTCGATTTTCACCCCTTACTACACCATTAAGACATTCTAGGCGCTA	300
ovi.vig	CGGACACAGACAAAATTCGATTTTCACCCCTTACTACACCATTAAGACATTCTAGGCGCTA	300
cap.cri	CAGACACAGACAAAATTCGATTTTCACCCCTTACTATACAATCAAAGACATTCTAGGCGCTA	300
ovi.mos	CAGACACAGACAAAATTCGATTTTCACCCCTTACTATACAATCAAAGACATTCTAGGCGCTA	300
ore.ame	CAGACCGAGACAAAATTCGATTTTCACCCCTTACTATACAATCAAAGACATTCTAGGCGCTA	300
cap.dor	CGGACCGAGACAAAATTCGATTTTCACCCCTTACTATACAATCAAAGACATTCTAGGCGCTA	300
cap.max	CAGACCGAGACAAAATTCGATTTTCACCCCTTACTATACAATCAAAGACATTCTAGGCGCTA	300
bis.bon	CAGACACAGACAAAATTCGATTTTCACCCCTTACTATACAATCAAAGACATTCTAGGCGCTA	300
bon.gru	CAGACCGAGACAAAATTCGATTTTCACCCCTTACTATACAATCAAAGACATTCTAGGCGCTA	300
bon.tsa	CAGACCGAGATAAAAATTCGATTTTCACCCCTTACTATACAATCAAAGACATTCTAGGCGCTA	300

bub.min	CAGACACAGACAAAAATCCCATTCACACCCCTACTACACCATTAAAGACATTCTAGGCGCCC	300
buba.bub	CAGACACAGACAAAAATCCCATTCACACCCCTATTACACCATTAAAGACATTCTAGGCGCCC	300
tra.ang	CAGACATAGACAAAAATCCCATTCACACCCCTATTACACTATCAAGGACATTCTAGGCGCCC	300
tra.eur	CRAACATAGACAAAAATCCCATTTCCACCCCTACTACACTATTAAGGACATTCTAGGCGCCC	300
kob.ell	CAGACATAGATAAAAAATCCCATTCACACCCCTACTACACCATCAAGACATTCTAGGCGCCC	300
kob.meg	CAGACACAGACAAAAATCCCATTCACACCCCATATTATACCATCAAGACATTCTAGGCGCCC	300
red.aru	CAGATGTAGACAAAAATCCCATTTTCATCCCTACTATACCTATCAAGGACATTCTAGGCGCCC	300
red.ful	CAGAYATGGACAAAAATCCCATTCACACCCCTACTACACCATCAAGACATTCTAGGCGCCC	300
neo.mos	CAGACGCAGACAAAAATCCCATTCACACCCCTACTACACCATTAAAGACATTCTAGGCGCCA	300
pel.cap	CCGACATAGACAAAAATCCCATTCACACCCCTACTACACCATTAAAGACATTCTAGGCGCCT	300
gaz.dam	CAGATGCCAGACAAAAATCCCATTCACACCCCTACTACACCATCAAGACATTCTAGGAGCAC	300
our.our	CAGATGCCAGACAAAGGTCCCATTCACACCCCTACTACACCATTAAAGACATTCTAGGCGCCT	300
ant.cer	CAGACGCAGACAAAAATCCCATTCACACCCCTACTACACTATCAAGACATTCTAGGAGCTC	300
sai.tat	CAGATTGAGACAAAAATCCCATTCACACCCCTACTACACCATTAAAGACATTCTAGGCGCCC	300
mad.kir	CAGACGCAGACGGAATCCCATTCACACCCCTACTACACTATTAAGACATTCTAGGCGCCC	300
rap.mel	CAGATATAGACAAAAATCCCATTTCCACCCCTACTACACCATTAAAGACATTCTAGGAGCCC	300
gaz.gaz	CAGACGCAGACAAAAATCCCATTTCCACCCCTACTACACCATCAAGGACATTCTAGGAGCAC	300
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hyd.ine	CAGATGCCAGATAAAAAATCCCATTTTCATCCCTACTACACCATTAAAGACATTCTAGGCGTAC	300
mun.mun	CAGATGTAGACAAAAATCCCATTTTCATCCCTACTATACCATTAAGACATTCTAGGCGCCC	300
alc.alc	CAGACGCAGACAAAAATCCCATTTTCACCCCTACTACACTATCAAGACATTCTAGGCGCCC	300
cer.ela.kan	CAGACGCAGACAAAAATCCCATTCCTTCCTTACTATACCATTAAGACATTCTAGGCGTCT	300
cer.ela.xan	CAGACGCAGACAAAAATCCCATTCCTTCCTTACTATACCATTAAGACATTCTAGGCGTCT	300
cer.ela.can	CAGACGCAGACAAAAATCCCATTCCTTCCTTACTATACCATTAAGACATTCTAGGCGTCT	300
cer.nip.cent	CGGACGCAGACAAAAATCCCATTCCTTCCTTACTACACCATTAAAGACATTCTAGGCGTCT	300
cer.nip.yes	CGGACGCAGACAAAAATCCCATTCCTTCCTTACTACACCATTAAAGACATTCTAGGCGTCT	300
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cer.nip.pul	CGGACGCAGACAAAAATCCCATTCCTTCCTTACTATACCATTAAGACATTCTAGGCGTCT	300
cer.nip.nip	CGGACGCAGACAAAAATCCCATTCCTTCCTTACTATACCATTAAGACATTCTAGGCGTCT	300
cer.ela.sco	CAGACGCAGACAAAAATCCCATTCCTTCCTTATTATACCATTAAGACATTCTAGGCGTCT	300
cer.dam	CAGATGTAGATAAAAAATCCCATTTTCATCCCTACTACACCATTAAAGACATTCTAGGCGTCT	300
ran.tar	CAGACTCAGATAAAAAATCCCATTCCTTCCTTATTATACCTATCAAGACATTCTAGGCGTCT	300
mos.fus	CAGATATAGACAAAAATCCCATTCACACCCCTACTACACCATCAAGACATTCTAGGCGTCT	300
mos.leu	CAGATATAGACAAAAATCCCATTCACACCCCTACTACACCATCAAGACATTCTAGGCGTCT	300
mos.chr	CAGACATAGACAAAAATCCCATTCACACCCCTACTACACTATCAAGACATTCTAGGCGTCT	300
mos.ber	CAGACATAGACAAAAATCCCATTCACACCCCTACTACACCATCAAGACATTCTAGGCGTCT	300
mos.mos	CAGACATAGACAAAAATCCCATTTCCACCCCTACTACACCATCAAGACATTCTAGGCGTCT	300
tra.jay	CAGACGCAGACAAAAATCCCATTCACACCCCTACTACACTATTAAGACATTCTAGGCGTCT	300
trag.nap	CAGACGCAGACAAAGATCCCATTCACACCCCTACTACACCATCAAGACATTCTAGGCGTCT	300
bala.acu	CTGACATAGACAAAAATCCCATTCACACCCCTACTACACAATCAAGACATTCTAGGCGCCC	300
bala.bon	CTGATATAGACAAAAATCCCATTCACACCCCTATTACACAATCAAGACATTCTAGGCGCCC	300
bala.bor	CCGACATAGACAAAAATCCCATTCACACCCCTACTACACAGTTAAAGACATTCTAGGCGCCC	300
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esch.rob	CTGACATAGATAAAAAATCCCATTCACACCCCTACTACACAATTAAGACATTCTAGGCGCCC	300
bala.mus	CCAACATAGACAAAAATCCCATTCACACCCCTACTACACAATTAAGACATTCTAGGCGCCC	300
mega.nov	CCAACATAGACAAAAATCCCATTCACACCCCTACTACACAATTAAGACATTCTAGGCGCCC	300
bala.phy	CCGACATAGATAAAAAATCCCATTCACACCCCTACCACACAATTAAGACATTCTAGGCGCCC	300
cap.mar	CCAACATAGACAAAAATCCCATTCACACCCCTACTACACAATTAAGACATTCTAGGCGCCC	300
ceph.com	CCAACATAGACATAATCCCATTCACACCCCTATTACACAATTAAGACATTCTAGGCGCCC	300
ceph.eut	CCAACATAGACATAATCCCATTCACACCCCTATTACACAATTAAGACATTCTAGGCGCCC	300
lage.obl	CCAACATAGACATAATCCCATTCACACCCCTATTACACAATTAAGACATTCTAGGCGCCC	300
ceph.heu	CCAACATAGACATAATCCCATTCACACCCCTATTACACAATTAAGACATTCTAGGCGCCC	300
ceph.heu	CCAACATAGACATAATCCCATTCACACCCCTATTACACAATTAAGACATTCTAGGCGCCC	300
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lage.scu	CCAACATAGACATAATCCCATTCACACCCCTACTACACAATTAAGACATTCTAGGCGCCC	300
lage.pbs	CCAACATAGACATAATCCCATTCACACCCCTATTACACAATTAAGACATTCTAGGCGCCC	300
liso.bor	CCAACATAGACATAATCCCATTCACACCCCTATTACACAATTAAGACATTCTAGGCGCCC	300
liso.por	CCAACATAGACATAATCCCATTCACACCCCTATTACACAATTAAGACATTCTAGGCGCCC	300

glo.mac	CCAACATAGACATAAATTC	300
glo.mel	CCAACATAGACATAAATTC	300
fere.att	CCAACATAGACATAAATTC	300
pepo.ele	CCAACATAGACATAAATTC	300
gram.gri	CCAACATAGACATAAATTC	300
pse.cra	CCAACATAGACATAAATTC	300
lage.acu	CTAACATAGATATAAATTC	300
orci.bre	CCAACATAGATATAAATTC	300
orca.bre	CCAACATAGACATAAATTC	300
del.cap	CCAATATAGACATAAATTC	300
del.tro	CCAACATAGACATAAATTC	300
del.del	CCAATATAGACATAAATTC	300
sten.cly	CCAATATAGACATAAATTC	300
sten.coe	CCAATATAGACATAAATTC	300
tur.adu	CCAATATAGACATAAATTC	300
sten.fro	CCAATATAGACATAAATTC	300
saus.chi	CCAACATAGACATAAATTC	300
sten.lon	CCAATATAGACATAAATTC	300
turs.tru	CCAACATAGATATAAATTC	300
lage.alb	CCAACATAGATATAAATTC	300
sten.bre	CCAACATAGATATAAATTC	300
sota.flu	CCAACATAGATATAAATTC	300
del.leu	CCAACATAGATATAAATTC	300
mono.mon	CCGACACTGACAAAATTC	300
plat.gan	CCGACACTGACAAAATTC	300
plat.min	CCGACATAGACAAAATTC	300
kogi.bre	CTGATATAGACAAAATTC	300
kogi.sim	CCAACATAGACAAAATTC	300
phys.cat	CTAACATAGACAAAATTC	300
lipo.vex	CTAACATAGACATAAATTC	300
phoc.sin	CCAATATAGATAAAAATTC	300
bera.bai	CCGATATAGACAAAATTC	300
ziph.car	CTGATATAGACAAAATTC	300
meso.eur	CCGACATAGATAAAAATTC	300
meso.bid	CTGACATAGATAAAAATTC	300
meso.den	CTGACATAGACAAAATTC	300
hype.amp	CTAACATAGATGCCATTC	300
meso.per	CAAACGCAGACAAAATTC	300
pent.bla	CTAACATAGACAAAATTC	300
hex.lib	CTAACACAGACAAAATTC	300
hipp.amp	CTAACATAGACAAAATTC	300
dic.sum	CTAACATAGACAAAATTC	300
rhin.son	CTAACATAGACAAAATTC	300
cera	CTAACATAGACAAAATTC	300
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baby.bab	CAGACATAGACAAAATTC	300
phac.afr	CAGACATAGACAAAATTC	300
sus.bar	CAGACATAGACAAAATTC	300
sus.scr.ewb3	CGGATATAGACAAAATTC	300
lama.gla	CGGATATAGACAAAATTC	300
lama.gua	CAGATATAGACAAAATTC	300
vic.vic	CAGACATAGACAAAATTC	300
cam.bac	CTGACTCAGACAAAATTC	300
acc.for	CTGACTCAGACAAAATTC	300
acc.gar	CTGACTCAGACAAAATTC	300
eum.jub	CTGACTCAGACAAAATTC	300
cal.cal	CTGACTCAGACAAAATTC	300
oda.sps	CTGACTCAGACAAAATTC	300

pho.fasciata	CCGACTCAGACAAAAATCCCATTTCCACCCCATACTATACAATTTAAAGATATCCTAGGAGCCC	300
pho.gro	CCGACTCAGACAAAAATCCCGCTCCACCCCATATTATACAATTTAAAGATATCCTAGGAGCCC	300
pho.vic	CCAACTCAGACAAAAATCCCATTTCCACCCGTACTATACAATTTAAAGATATCCTAGGGGCCC	300
cys.cri	CCGACTCAGACAAAAATCCCATTTCCACCCCATACTATACAATTTAAAGACATCCTAGGAGCCC	300
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lep.wed	CTGACTCAGACAAAAATCCCATTTCCACCCGTACTATACAATTTAAAGATATCCTAGGAGCCC	300
mir.leo	CCGACTCAGACAAAAATCCCATTTCCACCCGTACTATACAATTTAAAGACATCCTAGGAGCCC	300
eri.bar	CCGACTCAGATAAAAAATCCCATTTCCACCCGTACTATACAGTCAAGGACATCCTAGGGGCTT	300
mon.sch	CCAACTCAGACAAAAATCCCATTTCCACCCCATACTATACAATTTAAAGACATTCTAGGAGCTT	300
hela.mal	CTGACTCAGACAAAAATCCCATTTCCACCCGTACTATACAATTTAAGGACATCCTAGGCGCCC	300
sel.thi	CCAACTCGGACAAAAATCCCATTTCCACCCCATACTATACAATTTAAAGACGCCCTAGGCGCCC	300
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gla.vol	CTGACTCAGACAAAAATCCCATTTCCACCCGTACTTTCTCAATTTAAAGATACCCCTAGGATTCT	300
hyl.pha	CCGATTTCAGACAAAAATTCCATTTCCACCCCATACTATTCAATTTAAAGATCTCCTAGGGGCCC	300
pet.set	CCGATTTCAGACAAAAATTCCATTTCCACCCCATACTATTCAATTTAAAGATCTCCTAGGGGCCC	300
bel.pea	CTGAATCTGATAAAAGTACCAATTCACCCCATCTTCCACAATTTAAAGACATTTTAGGAGCAC	300
pte.mom	CCGAATCCGACAAAAATTCCATTTCCACCCGTACTTTCCACAATTTAAAGACATTTTAGGAGCAC	300
gala.demi	CAGACTCAGACAAAAATCCCATTTCCACCCGTATTACATAATTTCAAGGATCTCCTAGGACTGA	300
pero.pot	CAGAATCAGACAAAAATCCCATTTCCACCCGTACTACACCACCAAAGACTTACTAGGAGCCA	300
gala.mat	CAGACTCCGACAAAAATTCCATTTCCACCCGTACTACACAATTTAAAGACCTACTAGGAGTAA	300
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nyc.cou	CAGACTCAGATAAAGATTCCATTTCCACCCGTACTACTCACTTAAAGACCTCCTAGGAGTGG	300
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gorr	CCCCTCTGACAAAAATTCACCTTCCACCCGTACTACACAATTTCAAGACGCCCTCGGCTTAC	300
homo	CCCCTTCCGATAAAAAATTCACCTTCCACCCGTACTACACAATTTCAAGACGCCCTCGGCTTAC	300
dug.dug	CCGACTCAGACAAAAATTCCATTTCCACCCCATATTATTTCAGTCAAGACCTCCTAGGCCTAT	300
ele.max	CAGACTCAGACAAAAATTCCATTTCCACCCGTACTATACTATCAAGACCTCCTAGGCCTAC	300
afr.con	CCAACTCAGATAAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGATATCCTAGGCCTAG	300
pavo.mut	CCAACTCAGACAAAAATTCCATTTCCACCCCATACTACTCCCTCAAAGATATCCTAGGCCTAA	300
tra.bly	CTAACTCTGACAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGATATCCTGGGTCTAA	300
tra.sat	CCAACTCTGACAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGATATCCTAGGCCTAA	300
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tra.tem	CTAACTCTGACAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGATATCCTAGGCCTAA	300
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cat.wal	CTAACTCCGACAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGATATCCTAGGCCTAG	300
cro.cro	CTAATTCCGACAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGACATCCTAGGCCTAG	300
sym.ree	CTAACTCTGACAAAAATTCCATTTCCACCCGTACTACTCTCTCAAAGATATCCTAGGCCTAG	300
bam.tho	CTAACTCCGACAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGACATCCTAGGCCTAG	300
fra.fra	CTGACTCTGACAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGACATCCTAGGCCTAG	300
ish.cru	CTAACTCTGACAAAAATTCCATTTCCACCCGTACTACTCCCTCAAAGACATCCTAGGCCTAG	300
ant.par	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
ant.vir	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.ant.ant	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
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gru.ant.sha	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.leu	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.can.pra	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
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gru.can.tub	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.can.can	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
gru.ame	CAAACCTCCGATAAAAAATTCCATTTCCACCCGTACTTTTCTTAAAGATATCCTAGGATTCA	300
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gru.mon      CAAACTGCGATAAAAATCCATTCCACCCCTATTTTTCCTTAAAAGATATCCTAGGATTCA 300
gru.nig      CAAACTGCGATAAAAATCCATTCCACCCCTATTTTTCCTTAAAAGATATCCTAGGATTCA 300
gru.jap      CAAACTGTGATAAAAATCCATTCCACCCCTATTTTTCCTTAAAAGATATCCTAGGATTCA 300
cic.boy      CAAACTGCGACAAAATCCATTCCACCCCTACTTCTCCCTCAAAGATATCCTAGGCTTCA 300
rhe.ame      CTCACCTGTGACAAAATCCATTCCACCCCTACTTCTCCCTCAAAGATATCCTAGGACTAG 300
ant.alb      CCAACTGCGACAAAATCCATTCCACCCCTACTTCTCCCTCAAAGGACATCCTAGGATTCA 300
fal.fam      CAAACTGCGATAAAAATCCATTCCATCCCTATTACTCTCTCAAAGACCTCCTAGGATTCA 300
fal.ver      CAAACTGCGACAAAATCCATTCCATCCCTACTACTCTCTCAAAGACCTTTTAGGAGTCA 300
fal.per      CAAATTGCGACAAAATCCATTCCACCCCTACTACTCTCTCAAAGATATCCTAGGATTCA 300
fal.spa      CAAACTGTGACAAAATCCATTCCACCCCTACTACTCTCTCAAAGACCTCCTAGGTTTCA 300
ayt.ame      CAGACTGCGACAAAATCCATTCCACCCCTACTTCTCCTTCAAAGACATCCTAGGATTCA 300
smi.sha      CTAACCTCCGATAAAAATCCATTCCACCCCTACTTCTCCATAAAAAGACATCCTAGGCTTTG 300
vid.cha      CAGACTGTGACAAAATCCATTCCACCCCTACTACACCACAAAAGGACATCCTAGGCTTCG 300
chry.pic     CAAACACTGACAAAATCCATTCCACCCCTATTTTCTCATATAAAGACCTTTTAGGCGTCA 300
emy.orb.kur  CAAACACCGATAAAAATCCCTTTCCATCCCTACTTCTCATACAAAAGACCTATTAGGACTCA 300
che.mud      CAAATACCGACAAAATCCCTTTCCACCCCTACTTCTCCTACAAAAGACCTTACTAGGACTCA 300
eum.egr      CTAGCACAGATAAGGTGCCATTCCACCCCTATTACACATACAAAAGACCTTCTTGGTTTCA 300
*          *          *          *          *          *          *          *

aep.mel      TATTAATAATTCTAGTCCCTAATACTCCTAGTACTATTTCATACCCGACCTACTAGGAGACC 360
ore.ore      TATTACTAATTCTAGCTTTTATTACTCTTAGTATTATTTCACACCTGACCTACTTGGAGACC 360
add.nas      TACTACTAATTCTAGTCCCTCATACTACTAGTATTATTTCACACCCGACCTACTTGGAGACC 360
ory.dam      TACTACTAATCCTAGCCCTTATGTTGCTAGTATTATTTCGACCCGACCTACTTGGAGACC 360
hip.equ      TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTACTTGGAGACC 360
alc.bus      TATTACTAATCCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
sig.lic      TATTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
bea.hun      TACTACTAATTCTAGCCCTCATATTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
dam.lun      TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
con.tau      TATTACTAATTCTAGCCCTAATACTACTAGTACTATTTCGCGCCCGATTACTTGGAGACC 360
amm.ler      TGCTACTAATCCTCACCCTCACACTACTAGTACTATTTCACCCCGATCTACTCGGGGACC 360
pse.nay      CACTGCTAATCCTCGCCCTGATATTACTAGTATTATTTCACCCCGACCTACTCGGAGACC 360
cap.ibe      TGCTACTAATTCTTGTCTAATAATTACTAGTACTATTTCACACCCGACCTACTCGGGGACC 360
hem.jem      TACTACTAATTCTTGTCTAATAATTACTAGTACTATTTCACCCCGACCTACTTGGAGACC 360
cap.fal      TACTACTAATTCTCGCCCTGATGCTACTAGTACTATTTCACACCTGACCTACTCGGAGACC 360
rup.pyr      TACTACTAATCCTCACCCTTATACTACTGGTACTATTTCACACCTGACCTACTCGGAGACC 360
rup.rup      TACTACTAATCCTCACCCTCATACTACTAGTACTATTTCACACCTGACCTACTCGGAGACC 360
nem.cau      TACTACTAATCCTCACCCTCATACTACTAGTACTATTTCACACCTGACCTACTCGGAGACC 360
bud.tax.tax  TACTACTAATCCTCGTCCCTCATGTTGCTAGTACTATTTCACCCCGACCTACTCGGAGACC 360
pan.hod      TACTACTAATCCTAATCCTCATATTACTAGTACTATTTCACCCCGACCTACTCGGAGACC 360
ovi.amm      TCCTACTAATCCTCACCCTCATACTACTAGTACTATTTCACGCGCTGACCTACTCGGAGACC 360
ovi.vig      TCCTACTAATCCTCATCCTCATGCTGCTAGTACTATTTCACGCGCTGACTACTTGGAGACC 360
cap.cri      TGCTACTAATCCTCACCCTCATACTACTAGTACTGTTTCACACCCGACCTACTCGGAGACC 360
ovi.mos      TACTACTAATCCTTACCCTTATACTACTAGTATTATTTCACACCCGACCTACTTGGAGACC 360
ore.ame      TACTACTCATCCTCACCCTTATACTACTAGTATTATTTCACCCCGACTTACTCGGAGACC 360
cep.dor      TACTACTCATTCTAGCCCTAATAATCCTAGTATTATTTCACCCCGACTTACTCGGAGACC 360
cep.max      TATTACTAATTCTAGCCCTAATAATCCTAGTACTATTTCACCCCGACTTACTCGGAGACC 360
bis.bon      TATTACTAATTCTAAGCTCTAATACTACTAGTACTATTTCGACCCGACCTCCTCGGAGACC 360
bos.gru      TATTACTAATTCTAGCCCTAATACTTCTGCTACTATTTCACACCTCGACCTCCTCGGAGACC 360
bos.tra      TACTACTTATTCTAGCCCTAATAATCTAGTACTATTTCGACCCGACCTCCTCGGAGACC 360
bub.min      TGCTATTAATCCTAGCCCTAATACTATTAGTACTATTTCACACCCGACCTCCTCGGGGACC 360
buba.bub     TACTATTAATCCTAGCCCTAATACTATTAGTACTATTTCGACCCGACCTCCTCGGGGACC 360
tra.ang      TACTATTAATCCTAGCCCTAATACTAGTACTATTTCGACCTGACCTCCTCGGAGACC 360
tra.eur      TACTGCTAATCCTAGCTCTAATACTGCTAGTACTATTTCGACCCGACCTCCTCGGAGACC 360
kob.ell      TACTACTAATCCTAGTCTCTAATACTGCTAGTCTATTTCGCGCCCGACCTACTTGGAGACC 360
kob.meg      TCCTATTAATCCTAATACTAATACTGCTAGTACTATTTCGCGCCCGACCTACTTGGAGACC 360
red.aru      TACTGCTAATCCTAGTCTCTAATACTGCTAGTATTTCGACCCGACCTACTCGGAGACC 360
red.ful      TACTACTAATCCTGCGCCCTAAGACTATTAGTACTATTTCGACCCGACCTACTCGGAGACC 360
neo.mos      TCCTACTAATTCTAGTCTCTAAGACTCTTAGTCTTTA TTTTCACTCTCACTTTTAGGAGACC 360

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pel.cap	TATTACTAATCCTAATCCTAACACTCCTAGTATTATTTACCCCTGACCTATTAGGAGACC	350
gaz.dam	TACTATTAATTTCTAGCCCTCATACTCCTAGTTCTATTTCACACCAGATCTGCTTGGAGACC	350
our.our	TCCTACTAATTTCTAGCCCTCATGCTCCTAGTCCTATTTCACACCAGACCTGCTTGGAGACC	350
ant.cer	TACTATTAATTTTAACCCCTATGCTTCTAGTCCTATTTCACCCGGACCTGCTTGGAGACC	350
sai.cac	TACTACTTATTCTAATCCTCATACTTCTAGTCCTATTTCACACCAGACCTGCTTGGAGACC	350
mad.kir	TACTACTAATTATAGCCCTCATACTCCTAGTTCTATTTCACACCAGACCTACTCGGAGACC	350
rap.mel	TCCTATTAATCCTAACCCCTATGCTTCTAGTTCTATTTCGACACCAGACCTACTCGGAGACC	350
gaz.gaz	TACTACTAATCCTAGTTCTTATACTCCTAGTTCTGTTCTCACCAGACCTACTCGGAGACC	350
ant.ame	TACTAATAATCTTAGCCCTAATAATACTAGTACTATTTCACACCAGACCTGTTAGGAGACC	350
hyd.ine	TCCTTCTAATTTCTTTTCTAATGTTATTAGTCCTATTTTCACCTGACCTGCTTGGAGACC	350
mun.mun	TACTTCTAATTTCTTTTCTAATAATTATTAGTATTATTTCCTACCAGACCTGCTCGGAGACC	350
alc.alc	TACTCTTAATCTTTTCTAATACTACTAGTACTCTTTTCACACCAGACCTGCTTGGAGACC	350
cer.ela.kan	TACTTCTAGTACTCTTCTAATAATTACTAGTATTATTTCGACACCAGACCTGCTTGGAGACC	350
cer.ela.xan	TACTTCTAGTACTCTTCTAATAATTACTAGTATTATTTCGACACCAGACCTGCTTGGAGACC	350
cer.ela.can	TACTTCTAATACTCTTCTAATAATTACTAGTATTATTTCGACACCAGATCTGCTTGGAGACC	350
cer.nip.cent	TACTTCTAGTACTCTTCTAATAATTACTAGTATTATTTCGACACCAGACCTGCTTGGAGACC	350
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cer.nip.pul	TACTTCTAGTACTCTTCTGATAATTACTAGTATTATTTCGACACCAGACCTGCTTGGAGACC	350
cer.nip.nip	TACTTCTAGTACTCTTCTGATAATTACTAGTATTATTTCGACACCAGACCTGCTTGGAGACC	350
cer.ela.sco	TACTTCTTGTACTCTTCTTAAATAATTACTAGTATTATTTCGACACCAGACCTACTTGGAGACC	350
cer.dam	TATTCCCTATTTCTCTTCTTAAATAACTAGTACTATTTGACACCAGACCTGCTTGGAGACC	350
ran.tar	TACTCCTAATTTCTCTTCTTATACTACTAGTATTATTTGACACCAGACCTACTAGGAGACC	350
mos.fus	TATTACTAATCTTAGTCTTAAATAACTAGTACTATTTCACACCTGATTTACTTGGAGACC	350
mos.leu	TATTACTAATCTTAGTCTTAAATAACTAGTACTATTTCACACCTGATTTACTTGGAGACC	350
mos.chr	TATTACTAATCTTAGTCTTAAATAACTAGTACTATTTCACACCTGATTTACTTGGAGACC	350
mos.ber	TAATACTAATCTTAGTCTTAAATACTAGTACTATTTCACACCTGATTTACTTGGAGACC	350
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tra.jav	TAGCCCTATTTCTAGCCCTAATACTACTAGTCTTATTTTCACCCGACCTACTTGGAGACC	350
trag.nap	TAGTCTAATACTAGTCTTCTTAAATACTAGTCTTATTTTCACCCGACCTGCTTGGAGACC	350
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bala.bon	TACTACTAATTTCTAACCCCTACTAATACTAACCCCTATTTCGACCCGACCTGCTTGGAGACC	350
bala.bor	TACTACTAATTTCTAACCCCTACTAATACTAACCCCTATTTCGACCCGACCTGCTTGGAGACC	350
bala.edi	TACTACTAATTTCTAACCCCTACTAATACTAACCCCTATTTCGACCCGACCTACTTGGAGACC	350
esch.rob	TGCTACTAATTTCTAACCCCTACTAATACTAACCCCTATTTCGACCCGACCTGCTCGGAGACC	350
bala.mus	TACTACTAATTTCTAACCCCTACTAATACTAACCCCTATTTCGACCCGACCTGCTCGGAGACC	350
mega.nov	TATTACTAATTTCTAACCCCTACTAATACTAACCCCTATTTCGACCCGACCTGCTTGGAGACC	350
bala.phy	TATTACTAATTTCTAACCCCTACTAATACTAACCCCTATTTCGACCCGACCTGCTTGGAGACC	350
cap.mar	TACTACTAATTTCTGACCCCTACTAATACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
ceph.com	TATTCTTAATTTCTAACCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
ceph.eut	TATTCTTAATTTCTAACCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
lage.obl	TATTCTTAATTTCTAACCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
ceph.hec	TATTCTTAATTTCTAGCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
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lage.cru	TATTCTTAATTTCTAGCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
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lisso.bor	TATTCTTAATTTCTAGCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
lisso.per	TATTCTTAATTTCTAGCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
glo.mac	TACTCTTAATTTCTAGCACTACTAACCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
glo.mel	TACTCTTAATTTCTAGCACTACTAACCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
fere.att	TACTCTTAATTTCTAGCACTACTAACCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
pepo.ele	TACTCTTAATTTCTAGCACTACTAACCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
gram.gri	TACTCTTAATTTCTAGCACTACTAACCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
pse.cra	TACTCTTAATTTCTAGCACTACTAACCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
lage.acu	TACTCTTAATTTCTAACCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
ordi.bre	TACTCTTAATTTCTAACCCCTACTAGCACTAACCCCTATTTCGACCCGACCTACTAGGAGACC	350
ordi.bre	TACTCTTAATTTCTAGTCTTACTAACAATAACCCCTATTTCGACCCGACCTACTAGGAGACC	350

del.cap	TACTCCTAATCTTAACCCCTACTAGCCTGACCCTATTCACTCCAGACCTACTAGGAGACC	360
del.tro	TACTCCTAATCTTAACCCCTACTAGCCTGACCCTATTCACTCCCGACCTACTAGGAGACC	360
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tur.adu	TACTCCTAATCTTAACCCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
sten.fro	TACTCCTAATCTTAACCCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
saus.chi	TACTCCTAATCTTAACCCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
sten.lon	TACTCCTAATCTTAACCCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
turs.tru	TACTCCTAATCTTAACCCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
lage.alb	TACTTTTAACTCTTAACCCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
sten.bre	TACTTTTAACTCTTAACCCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
sota.flu	TACTCCTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
del.leu	TACTACTAATCTCTAACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
mono.mon	TCCTACTAATCTCTAACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
plat.gan	TCATCCTAATCTCTAACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
plat.min	TCATCCTAATCTCTAACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
kogi.bre	TACTGCTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
kogi.sim	TACTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
phys.cat	TACTACTAATCTCTAACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
lipo.vex	TTCTATTAAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
phoc.sin	TACTATTAAATCTCTAACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
bera.bai	TACTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
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meso.eur	TACTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
meso.bid	TACTACTAATCTCTAACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
meso.den	TACTATTAAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
hype.amp	TATTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
meso.per	TATTATTAAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
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hipp.amp	TACTCCTAATAAATACTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
dic.sum	TACTTTCTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
rhin.sen	TGCTTCTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
cera	TACTCCTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
equu	TCCTCCTAGTCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
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phac.afs	TATTCTAATAAATACTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
sus.bar	TATTTATAAATACTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
sus.scr.ewb1	TATTTATAAATACTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
lama.gla	TACTACTTATTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
lama.gua	TACTACTTATTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
vic.vic	TACTACTTATTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
cam.bac	TCCTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
arc.for	TCCTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
arc.gaz	TCCTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
eum.jub	TCCTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
zal.cal	TCCTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
odo.ros	TCCTACTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
pho.fasciata	TACTCCTCATCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
pho.gro	TACTCCTCATCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
pho.vic	TACTCCTCATCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
rys.cri	TACTCCTCATCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
nyd.lep	TATTCCTCATCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
lep.wed	TACTCCTCATCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
nir.leo	TACTTTCTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
cri.bar	TACTTTCTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
non.nch	TACTCCTAATCTCTGACCCTACTAGCCTAACCCTATTCACTCCCGACCTACTAGGAGACC	360

hela.mal	TACTTCTTACCGCTAGCCCTAACAAACCTAGTTCTATTTCTCCGCCGACCTAACAGAGAGACC	357
sel.thi	TACTTCTCATCGCTAGCCCTAGCAACTCTAGTCTCTATTCTCCGCCGACTTACTAGGAGAGACC	358
ail.ful	TACTCCTTATCGCTAATTCTCATGACATTAGTACTATTCTTACCTGACTTCTCTGGTGTATC	359
fel	TAGTACTAGTTTAAACACTCATACTACTCTCTCTATTTTCACCAGACCTGCTAGGAGAGACC	360
can	TACTCCTACTCGCTAATCGCTAATATGACTAGTTTTATTTTCACCTGACCTATTAGGAGAGACC	361
tal	TAATCGCTAATTATAGCTCTATCATCATTAGTATTTATTTTCACCTGACCTACTAGGAGAGACC	362
gla.sab	TAATCGCTCATCTTAACTCTTCATAAACCGCTAGTTCTCTTCACCCCGCTGATCTTTTAGGAGAGACC	363
gla.vol	TAATCGCTTATCTTAACTCTTCATAAACCGCTAGTTCTCTTCACCCCGGATCTTTTAGGAGAGACC	364
hyl.pha	TTATTCTCTCTCGCTAATCTTTATAAACTTAGTACTATTCTCCCGCGATCTTTTAGGAGAGACC	365
pec.sec	TTATTCTCTCTCGCTAATCTTTATAAACTTAGTACTATTCTCCCGCGATCTTTTAGGAGAGACC	366
bel.pea	TAATCTCTCCCGCTTATATTATTAACAAACCTATTTCTATTCTCCCGCGTGTCTCTTAGGAGAGACC	367
pte.mem	TTCTCTCTCTCCCGCTCTCTATTGATAATCTTAGTCTCTCTTTACTCCAGACCTCTCTTAGGAGAGACC	368
gala.demi	TTATTCTCTCTACTAAGCTCTGTTCTCTCTCTAGTAAATATTCTCTCCCGGACCTGCTAGGAGAGACC	369
pero.pot	TTCTCTCTCTACTAATCTCTACTCAGCCTAGTCTCTATTCTCTCCCGAGACCTATTAGGAGAGACC	370
gala.mat	TTCTCTTACTACTATGCGCTATTCTCTCTAGTACTATTCTCTCCCGGATCTGTTAGGAGAGACC	371
gala.moh	TTCTCTTACTATTATCGCTATTCTCTCTAGTACTATTCTCTCCCGTACCTGCTGGGAGAGACC	372
oco.gar	TTCTCTCTCTCTTAAACCGCTATTCTCTCTAGTCTCTATTCTCTCCCGGACCTCTTAGGAGAGACC	373
lor.tar	TTGCTCTCTTAAATCAGCTTATCTACTCTAGTCTCTATTCTCTCCCGTACCTTTTAGGAGAGACC	374
nyc.cou	TTTTCTCTATTAGCAACCGCTATCTATTCTAGTCTTATTCTCTCCCGTACCTCTTAGGAGAGACC	375
mus	TAATCATACTCTTAACTCTCATAAACCGCTAGTATTATTCTCTCCAGACATACTAGGAGAGACC	376
gorr	TTCTCTTTCTCTGACCTTGATAACATTAACACTATTCTCACCAGACCTCTTAGGAGAGACC	377
homo	TTCTCTCTCTCTCTCTCTTAAATGACATTAACACTATTCTCACCAGACCTCTTAGGAGAGACC	378
dug.dug	TTCTCTCTCTCTCTCTCTTAAATGACATTAACACTATTCTCACCAGACCTCTTAGGAGAGACC	379
ele.max	TTATCTCTATTCTTACTCTCTCTCTACTCTTAGCCCTACTATCTCCAGACATACTAGGAGAGACC	380
afr.con	CACTCATGCTCATTCGATTCCTGACACTAGCCCTACTCTCTCCCGCAACCTCTTAGGAGAGACC	381
pavo.mut	CTCTTATATTATCTCCATTCCTTACACTAGCCCTATTCTCTCCCGCAACCTCTTAGGAGAGACC	382
tra.bly	CACTCATGCTCAGCCCGCTCTCTCAGACTAGGCTATTCTCTCACCAGAACCTATTAGGAGAGACC	383
tra.sac	CACTCATGCTCAGCCCGCTCTCTCAGACTAGGCTATTCTCTCACCAGAACCTATTAGGAGAGACC	384
tra.cob	CACTCATACTCATCTCTCTCTCTCAGACTAGGCTATTCTCTCACCAGAACCTATTAGGAGAGACC	385
tra.tem	CACTCATACTCATCTCTCTCTCTCAGACTAGGCTATTCTCTCACCAGAACCTATTAGGAGAGACC	386
arg.arg	CACTCATACTCTCTCTCTCTCTTACACTAAGCCCTATTCTCTCACCAGAACCTATTAGGAGAGACC	387
cat.wal	CACTTATATTACCCCACTCTCTTAACTAGCCCTATTCTCTCACCAGAACCTATTAGGAGAGACC	388
cro.cro	CACTTATACTCAGCCCACTCTCTTAACTAGCCCTATTCTCTCACCAGAACCTATTAGGAGAGACC	389
sym.ree	CACTTATACTCAGCCCACTCTCTTAACTAGCCCTATTCTCTCACCAGAACCTATTAGGAGAGACC	390
bam.cho	CCCTTATATTCTATCCCTCTCTCTTACACTAGCCCTATTCTCTCCCGTAACTCTTAGGAGAGACC	391
fra.fra	CCCTTATATTCTATCCCTCTCTCTTACACTAGCCCTATTCTCTCCCGTAACTCTTAGGAGAGACC	392
ish.cru	CACTTATACTCATCTCCCTCTCTCTTACACTAGGCTATTCTCTCCCGTAACTCTTAGGAGAGACC	393
ant.par	TACTCATACTACTCTCCACTCATAAACCTAGCTCTATTCTCTCACCAGAACCTACTAGGAGAGACC	394
ant.vir	TACTCATACTACTCTCCACTCATAAACCTAGCTCTATTCTCTCACCAGAACCTACTAGGAGAGACC	395
gru.ans.ans	CACTCATACTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	396
gru.ans.gil	CACTCATACTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	397
gru.ans.sha	CACTCATACTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	398
gru.leu	TACTCATACTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	399
gru.can.pra	TACTCATACTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	400
gru.can.cow	TACTCATACTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	401
gru.can.tab	TACTCATACTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	402
gru.can.can	TACTCATACTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	403
gru.ame	TACTCATATTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	404
gru.gru	TACTCATATTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	405
gru.mon	TATTGATATTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	406
gru.nig	TATTGATATTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	407
gru.jap	CACTCATATTACTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	408
dis.boy	CACTCTCTACTCTCTCCACTCATAAACCTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	409
che.ame	CTCTCATATTATCTCCCGCTCTTAACTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	410
ant.alb	CAGTAATACTCTCTCTCTTAACTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	411
tal.fam	TACTCATATAGCTCTCCCGCTTAACTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	412
tal.vuc	TACTCATATAGCTCTCCCGCTTAACTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	413
tal.por	TACTCATATAGCTCTCCCGCTTAACTAGGCTATTCTCTCACCAGAACCTACTAGGAGAGACC	414

fal.spa TGCTCATACTCCTGCCCCCTAATAGCCCTAGCCCTATTACCCCCAAACCTGCTAGGAGACC 360  
 ayt.ame TCCTCATGCTCACCCCCCTAATAGCACTAGCCCTATTCTCACCACAAACCTCCTAGGAGACC 360  
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 vid.cha TACTAATATTCCGACTCCTAGCTTCCATAGCCCTATTCTCCCCAAACATACTAGGAGATC 360  
 chry.pic TTCTAATACTAACCCCTCCTACTAACCCCTAACACTATTCTCTCCTAACCTTCTAGGAGACC 360  
 emy.orb.kur TCCTAATACTAGCCCTCCTGCTAACCCCTAACACTATTCTCTCCTAACCTTCTAGGAGACC 360  
 che.mud TTTTAATACTAACTTTCTCCTAACCTTAACACTTTTCTCCCCCTACTTACTAGGAGACC 360  
 eum.egr TCATTATACTGTCTGTTCTACTAGCCCTCGCCCTTTTCTCACCACAAACCTTCTAGGAGACC 360

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 ore.ore CAGATAACTACACCCCGCAACCCACTCAACACTCCCCCTCACATTAACCCAGAATGGT 420  
 add.nas CAGACAATTATACCCCGCAAAATCCACTTAGCAGCCCCCTCACATCAAAACCTGAATGAT 420  
 ory.dam CAGATAATTATACACCAGCAAAATCCACTTAACACACCCCTCACATCAAAACCCGAATGAT 420  
 hip.equ CAGACAACTATGCCCCAGCAAAACCCACTCAACACGGCCCCCTCACATTAACCCCGAATGAT 420  
 alc.bus CAGACAACTACACCCCGCGAACCCTTAACACACCCCTCACATCAAGCCCCGAATGAT 420  
 sig.lic CAGACAACTACACCCCGCGAACCCTTAACACACCCCTCACATCAAGCCCCGAATGAT 420  
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 dam.lun CAGACAACTACACCCCTGCAAAACCCACTCAACACGCCCCCTCACATCAAGCCCCGAGTGT 420  
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 cap.ibe CAGACAACTATACCCCGCAAAACCCACTCAATACACCCCTCACATTAACCCGAATGAT 420  
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 cap.fal CAGATAACTATATCCCGCAAAATCCACTCAATACACCCCTCATATCAAAACCTGAGTGGT 420  
 rup.pyr CAGATAACTATACCCCGCGAACCCTCAACACACCCCTCACATCAAAACCCGAATGAT 420  
 rup.rup CAGATAATTACACCCCGCGAACCCTCAACACACCCCTCACATTAACCCGAGTGT 420  
 nem.cau CAGACAACTATACCCCGCAAAACCCACTCAGCACACCCCTCACATTAACCCGAATGAT 420  
 bud.tax.tax CAGATAATTATACCCCGCAAAATCCACTCAACACACCCCTCACATTAACCCGAATGAT 420  
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 cep.dor CAGATAACTACACCCCGCAAAACCCACTCAACACACCTCCCCATATTAACCCCGAATGAT 420  
 cep.max CAGATAATTATCTCCAGCAAAACCCACTTAACACACCTCCCCATATCAAAACCCGAATGAT 420  
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 bos.gru CAGACAACTACACCCCGCAAAATCCACTCAACACACCTCCCCATATCAAAACCCGAATGAT 420  
 bos.tra CAGACAACTACACCCCGCAAAACCCACTTAGCACACCTCCCCATATTAAGCCCCGAATGGT 420  
 bub.min CAGACAACTACACCCCGCAAAACCCACTCAACACACCTCCCCATATCAAAACCTGAATGGT 420  
 bub.bub CAGACAACTACACCCCGCAAAACCCACTCAACACACCTCCCCATATCAAGCCTGAATGGT 420  
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 tra.eur CCGACAACTACACCCCGCGAACCCTCAACACACCTCATATCAAAACCTGAATGAT 420  
 kob.ell CTGACAATTATGCCCCAGCAAAACCCACTTAACACGCCCCCTCACAATTAACCCGAATGAT 420  
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 red.aru CCGACAATTATCTCCAGCAAAATCCACTCAACACACCCCTCATATTAACCCCGAATGAT 420  
 red.ful CCGACAATTATACACCCCGCAAAACCCACTCAACACACCCCTCACATCAAAACCGAATGGT 420  
 neo.mos CAGACAACTACACCCCGCAAAACCCCTCTTAACACGCCCCCTCCCCATATCAAAACCCGAATGAT 420  
 pel.cap CTGACAATTATACCCCTGCAAAACCCGCTCAACACACCCCTCATATCAAAACCCGAATGAT 420  
 gaz.dam CAGACAACTACACACCCAGCAAAATCCACTCAATACACCCCTCATATTAAGCCTGAGCGAT 420  
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 sai.tat CAGACAACTACACRCAGCAAAACCCACTTAACACACCCCTCATATTAACCCCGAATGAT 420  
 mad.kir CAGACAACTACACACCAGCAAAATCCCTTAACACGCCCCCTCACATTAACCCGAATGAT 420  
 rap.mel CAGACAACTATACACCAGCAAAACCCACTCAACACACCCCTCATATCAAAACCCGAATGGT 420  
 gaz.gaz CAGACAACTATACACCAGCAAAATCCACTCAACACACCCCTCACATCAAAACCTGAATGGT 420  
 ant.ame CCGACAACTACACACCAGCTAACCCACTCAACACTCCCCCACACAATTAAGCCGAGAATGAT 420



aep.mel	ACTTCCTGTTNGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ore.ore	ATTTCCTATTNGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
add.nas	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
ory.dam	ATTTCCTATTGTCATATGCGATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
hip.equ	ATTTCCTATTGTCGATGCGCAATCCTACGATCGATCCCCAATAAGCTGGGAGG	472
alc.bus	ATTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
sig.lic	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
bea.hun	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
dam.lun	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
con.tau	ACTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACGGACTAGGAGG	472
amm.ler	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAATAAACTGGGAGG	472
pse.nay	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAAGCTAGGAGG	472
cap.ibe	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
hem.jem	ATTTCCTATTGTCATACGCGATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
cap.fal	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
rup.pyr	ATTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTGGGAGG	472
rup.rup	ATTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTGGGAGG	472
nem.cau	ATTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
bud.tax.tax	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
pan.hod	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
ovi.amm	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
ovi.vig	ACTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
cap.cri	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
ovi.mos	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
ore.ame	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
cep.dor	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
cep.max	ATTTCCTATTGTCGATGCGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
bis.bon	ACTTCCTATTGTCATANGCAATTTTACGGTCAATCCCCAACAATAAACTAGGAGG	472
bos.gru	ACTTCCTATTGTCATACGCAATTTTACGGTCAATCCCCAACAATAAACTAGGAGG	472
bos.tra	ATTTCCTGTTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
bub.min	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
buba.bub	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
tra.ang	ATTTCCTGTTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
tra.eur	ACTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
kob.ell	ACTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
kob.meg	ATTTCCTATTGTCATACGCAATTTTACGGTCAATCCCCAACAATAAACTAGGAGG	472
red.aru	ACTTCCTATTGTCATATGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
red.ful	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
neo.mos	ACTTTTTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
pel.cap	ATTTCCTATTGTCATATGCGATTTCTACGATCAATCCCCAACAATAAACTAGGAGG	472
gaz.dam	ATTTCCTATTGTCATACGCAATTTCTCGGATCAATCCCCAACAATAAACTAGGAGG	472
our.our	ATTTCCTATTGTCATACGCAATTTCTCGGATCAATCCCCAACAATAAACTAGGAGG	472
ant.cer	ACTTCCTATTGTCATACGCAATCCTCGGATCAATCCCCAACAATAAACTAGGAGG	472
sai.sat	ACTTCCTATTGTCATACGCAATCCTCGGATCAATCCCCAACAATAAACTAGGAGG	472
mad.kir	ATTTCCTATTGTCATATGCAATCCTCGGATCAATCCCCAACAATAAACTAGGAGG	472
rap.mel	ATTTCCTATTGTCATATGCAATTTCTCGGATCAATCCCCAACAATAAACTAGGAGG	472
gaz.gaz	ACTTCCTATTGTCATATGCAATTTCTCGGATCAATCCCCAACAATAAACTAGGAGG	472
ant.ame	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
hyd.ine	ATTTCCTATTGTCATACGCAATTTCTACGATCAATCCCCAACAATAAACTAGGAGG	472
mun.mun	ATTTCCTATTGTCATACGCTATTCTACGATCAATCCCCAACAATAAACTAGGAGG	472
alc.alc	ATTTCCTATTGTCATACGCAATTTCTACGATCAATCCCCAACAATAAACTAGGAGG	472
cer.ela.kan	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
cer.ela.kan	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
cer.ela.gan	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
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cer.nip.yes	ACTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472
cer.nip.ker	ATTTCCTATTGTCATACGCAATCCTACGATCAATCCCCAACAATAAACTAGGAGG	472



hyd.ine	CAGACAATTATACTCCAGCAAACCCACTCAATACACCCCCCTCACATTTAAACCAGAATGAT	410
mun.mun	CCGACAATTATACCCAGCAAACCCACTCAATACACCCCCCTCACATCAAACCTGAATGAT	420
alc.alc	CAGACAACCTACACCCAGCTAATCCACTCAACACACCCCCCTCATATTTAAACCTGAATGGT	420
cer.ela.kan	CAGACAACCTATACCCAGCAAATCCACTCAATACACCCCCCTCACATTTAAACCTGAATGAT	420
cer.ela.xan	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTTAAACCTGAATGAT	420
cer.ela.can	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTTAAACCTGAATGAT	420
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cer.nip.ker	CAGACAACCTACACCCAGCAAATCCGCTCAACACACCCCCCTCACATCAAACCTGAATGAT	420
cer.nip.pul	CAGACAACCTACACCCAGCAAATCCGCTCAACACACCCCCCTCACATCAAACCTGAATGAT	420
cer.nip.nip	CAGACAACCTACACCCAGCAAATCCGCTCAACACACCCCCCTCATATTTAAACCTGAATGAT	420
cer.ela.sco	CAGATAACTACACCCAGCAAACCCACTCAACACACCTCCTCATATTTAAACCCGAATGAT	420
cer.dam	CAGACAACCTATACCCAGCAAACCCACTCAACACTCCCCCTCATATTTAAACCTGAATGAT	420
ran.tar	CGGACAATTATACCCAGCAAACCCATTAAATACGCCCCCAGATATTTAAACCCGAATGAT	420
mos.fus	CGGACAATTATACCCAGCAAACCCATTAAATACGCCCCCAGATATTTAAACCCGAATGAT	420
mos.leu	CGGACAATTATACCCAGCAAACCCATTAAATACGCCCCCAGATATTTAAACCCGAATGAT	420
mos.chr	CGGACAATTATACCCAGCAAACCCATTAAACACACCCAGCAGATTTAAACCCGAATGAT	420
mos.ber	CGGACAATTATACCCAGCAAACCCATTAAATACACCTCCAGATATTTAAACCCGAATGGT	420
mos.mos	CGGACAACCTATACCTCCAGCAAACCCATTAAATACACCTCCAGATATTTAAACCCGAATGGT	420
tra.jav	CAGATAACTACACCCCGGCAACCCCTTAACACACACCCCATATCAAACCCGAATGAT	420
trag.nap	CCGACAATTACACTCCGGCAAACCCCTCAACACACACCTCATATTTAAAGCCAGAGTGGT	420
bala.acu	CCGACAACCTATACCCAGCAAACCCACTCAGTACCCAGCAGACATTTAAACCCAGAATGAT	420
bala.bon	CCGACAACCTACACCCAGCAAACCCACTCAGTACCCAGCAGCAGATTTAAACCCAGAATGAT	420
bala.bor	CAGACAACCTACACCCAGCAAATCCACTCAGTACCCAGCAGCAGATTTAAACCCAGAATGAT	420
bala.edi	CAGACAACCTACACTCCAGCAAATCCACTCAGTACCCCAACACACATTTAAACCCAGAATGAT	420
esch.rob	CAGACAACCTATACCCAGCAAACCCACTCAGCACCCTAACACATATTTAAACCCAGAGTGGT	420
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mega.nov	CAGATAACTACACCCAGCAAACCCACTCAGTACCCAGCAGCAGATTTAAACCCAGAGTGGT	420
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cap.mar	CTGACAACCTACACCCAGCAAATCCCTCAGCACCCAGCAGACATCAAAGCCAGAATGAT	420
ceph.com	CTGATAACTATACCCAGCAAATCCATTAAAGCACCCCTGCACACATCAAACCCAGAATGAT	420
ceph.eut	CTGATAACTATACCCAGCAAATCCATTAAAGCACCCCTGCACACATCAAACCCAGAATGGT	420
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glo.mel	CTGATAACTATACCTCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCCAGAATGGT	420
fere.att	CTGATAACTATACCTCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCCAGAATGGT	420
pepo.ele	CTAACAACCTATACCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCCAGAATGGT	420
gram.gri	CTGATAACTACACTCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCCAGAATGGT	420
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sten.coe	CTGATAACTATACCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCCAGAATGGT	420
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sten.fro	CTGACAATTATACCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCCAGAATGGT	420
aus.chi	CCGATAACTATACCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCCAGAATGGT	420
sten.lon	CTGATAACTATACCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCCAGAATGGT	420



kogi.sim	ACTTTCTATTTCGCATACGCCATTCTACGATCAATTCCCTAACAAAAGTGGGAGG	472
phys.cat	ATTTCCCTATTTCGCGTACGCCATCCTACGATCTGTCCCCAATAAACTAGGAGG	472
lipo.vex	ATTTCCCTCTTCGCATACGCCAATTCTACGATCAATTCCCAATAAACTAGGAGG	472
phoc.sin	ATTTCCCTCTTCGCATACGCCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bera.bai	ACTTCCTGTTTCGCATACGCCAATCTTACGATCAGTCCCTAATAAACTAGGGGG	472
ziph.car	ACTTCCTATTTCGCATACGCCAATCCTACGATCAATTCCCAATAAACTAGGAGG	472
meso.eur	ACTTCCTATTTCGCATATGCAATTCTTACGATCAATTCCCAATAAACTAGGAGG	472
meso.bid	ATTTCCCTATTTCGCATACGCCAATCTTACGATCAATTCCCAATAAACTAGGAGG	472
meso.den	ATTTTCTATTTCGCATACGCCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
hype.amp	ACTTCCTATTTCGCATACGCCAATCCTACGTTCAATCCCTAACAAACTAGGAGG	472
meso.per	ATTTTCTATTTCGCATATGCAATTTTACGATCAGTTCCCTAATAAACTAGGAGG	472
pont.bla	ATTTCCCTATTTCGCCTACGCCATCCTACGATCAATTCCCAATAAACTGGGAGG	472
hex.lib	ATTTCCCTGTTTCGCATACGCCAATCTCCGATCAATCCCTAACAAACTGGGAGG	472
hipp.amp	ATTTCCCTGTTTCGCGTACGCGATTCTCCGATCAATCCCCAATAAACTAGGAGG	472
dic.sum	ACTTCCTATTTCGCCTACGCCAATCCTACGATCCATCCCCAATAAACTAGGCCG	472
rhin.son	ATTTCCCTATTTCGCTTACGCCAATCCTACGATCCATCCCCAATAAACTAGGCCG	472
cera	ACTTTCTATTTCGCTTACGCCAATCCTACGATCCATCCCTAACAAACTAGGCCG	472
equu	ATTTCCCTATTTCGCTTACGCCAATCCTACGCTCCATCCCAATAAACTAGGTGG	472
baby.bab	ACTTCCTATTTCGCTACGCCATCCTACGCTCAATCCCCAATAAACTAGGTGG	472
phac.afr	ACTTCCTATTTCGCTACGCCATCCTACGTTCAATCCCTAATAAACTAGGTGG	472
sus.bar	ACTTCCTATTTCGCTACGCTATTCTACGTTCAATCCCTAATAAACTAGGTGG	472
sus.scr.ewb3	ATTTCTTATTTCGCTACGCTATTCTACGTTCAATCCCTAATAAACTAGGTGG	472
lama.gla	ACTTCCTATTTCGCTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG	472
lama.gua	ACTTCCTATTTCGCATATGCCATCCTACGATCCATCCCCAATAAACTAGGTGG	472
vic.vic	ATTTCCCTATTTCGCATATGCTATTCTACGATCGATCCCCAATAAACTAGGTGG	472
cam.bac	ATTTCCCTATTTCGCATACGCTATCCTACGATCCATCCCCAATAAACTAGGTGG	472
arc.for	ATTTTCTATTTCGCTTACGCCAATTTTACGATCTATCCCCAATAAACTAGGTGG	472
arc.gaz	ATTTTCTATTTCGCTATGCCAATTTTACGATCTATCCCCAATAAACTAGGTGG	472
eum.jub	ATTTCCCTATTTCGCTATGCTATTTTACGATCCATCCCCAATAAACTAGGTGG	472
zal.cal	ATTTCCCTATTTCGCTATGCTATTTTACGATCCATCCCCAATAAACTAGGTGG	472
odo.ros	ATTTCCCTATTTCGCTACGCTATCCTCCGATCTATCCCCAATAAACTAGGTGG	472
pho.fasciata	ACTTTCTATTTCGCTACGCCAATCCTACGATCAATCCCCAATAAACTAGGTGG	472
pho.gro	ACTTTTCTATTTCGCTACGCCAATCCTACGATCAATCCCCAATAAACTAGGTGG	472
pho.vit	ACTTCCTATTTCGCTACGCCAATCCTACGATCCATCCCCAATAAACTAGGTGG	472
cys.cri	ACTTCCTATTTCGCTATGCAATCCTACGATCTATCCCCAATAAACTAGGTGG	472
hyd.lep	ATTTCCCTATTTCGCTACGCCAATCCTACGATCCATCCCCAATAAACTAGGTGG	472
lep.wed	ATTTCCCTATTTCGCTACGCCAATCCTACGATCCATCCCCAATAAACTAGGTGG	472
mir.leo	ATTTCCCTATTTCGCTACGCCAATCCTACGATCTATCCCCAATAAACTAGGTGG	472
eri.bar	ATTTCCCTATTTCGCTATGCAATCCTACGATCCATCCCCAATAAACTAGGTGG	472
mon.sch	ACTTCCTATTTCGCTACGCCAATCCTACGATCCATCCCCAATAAACTAGGTGG	472
hela.mal	ACTTTCTATTTCGCTACGCCAATCCTACGATCCATCCCCAATAAACTAGGTGG	472
sel.chi	ACTTTTCTATTTCGCTATGCAATCCTACGATCCATCCCCAATAAACTAGGTGG	472
ail.ful	ATTTCCCTATTTCGCATATGCAATCTACGATCCATCCCCAATAAACTAGGTGG	472
fel	ACTTCCTATTTCGCATACGCCAATCTCCGATCCATCCCCAATAAACTAGGTGG	472
can	ATTTTCTATTTCGCTATGCTATCCTACGATCCATCCCCAATAAACTAGGTGG	472
tal	ACTTCCTATTTCGCATATGCCATCCTACGATCAATTCCTAATAAACTAGGTGG	472
gla.sab	ACTTTCTATTTCGCATACGCCAATCTACGATCTATCCCCAATAAACTAGGTGG	472
gla.vol	ACTTTTCTATTTCGCTATGCAATCTACGATCTATCCCCAATAAACTAGGTGG	472
hyl.pha	ACTTTCTATTTCGCATACGCCAATCCTACGATCTATCCCCAATAAACTAGGTGG	472
pet.set	ACTTTCTATTTCGCATACGCCAATCCTACGATCTATCCCCAATAAACTAGGTGG	472
bel.pea	ACTTTTCTAATTTATTACGCCAATCCTTCGATCCATCCCCAATAAACTAGGTGG	472
pte.mom	ATTTCCCTATTTCGCATATGCTATCCTACGATCTATCCCCAATAAACTAGGTGG	472
gala.demi	ATTTCCCTATTTCGCTACGCCATCCTACGATCTATCCCCAATAAACTAGGTGG	472
pero.poc	ACTTTCTATTTCGCTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG	472
gala.mat	ACTTCCTATTTCGCTTATGCTATCCTACGATCCATCCCCAATAAACTAGGTGG	472
gala.mon	ACTTCCTATTTCGCTACGCCATCCTTCGATCAATCCCCAATAAACTAGGTGG	472
oto.gar	ATTTCCCTATTTCGCTATGCTATCCTACGATCCATCCCCAATAAACTAGGTGG	472
lor.car	ATTTCCCTATTTCGCATACGCCAATCCTACGATCAATCCCCAATAAACTAGGTGG	472

nyc.cou	ATTTTCTATTTCGGCTACGCCATCCTTCGATCAATCCCCAACAACTAGGAGG	472
mus	ATTTTCTATTTCGCATACGCCATTCTACGCTCAATCCCCAATAAACTAGGAGG	472
gorr	ATTTTCTATTTCGGCTACGCCAATTCTCCGATCTGTCCCCAATAAACTAGGAGG	472
homo	ATTTTCTATTTCGGCTACACAAATCTCCGATCCGCTCCCTAACAAACTAGGAGG	472
dug.dug	ACTTTTCTATTTCGGATACGCTATCCTCCGATCTATCCCTAATAAACTAGGCGG	472
ele.max	ACTTTCTTTTTTGCTTACGCCATTCTACGATCTGTACCAAAACAAACTAGGAGG	472
afr.con	ATTTTCTATTTCGGCTATGCCATCCTTCGCTCAATCCCCAACAAACTAGGAGG	472
pavo.mut	ACTTTCTATTTCGGCTACGCCATCCTTCGTTCAATCCCCAACAAACTAGGAGG	472
tra.bly	ACTTTCTATTTCGGCTACGCCATCCTTCGCTCAATCCCCAACAAACTTGGGAGG	472
tra.sat	ACTTTCTATTTCGGCTATGCCATCCTACGCTCAATCCCCAACAAACTCGGAGG	472
tra.cob	ATTTTCTGTTTCGCTTATGCCATCCTACGCTCAATCCCCAACAAACTCGGAGG	472
tra.tem	ATTTTCTGTTTCGCTTATGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
arg.arg	ACTTTCTATTTCGGCTATGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
cat.wal	ACTTTCTATTTCGGCTACGCTATCCTACGCTCAATCCCCAATAAACTCGGAGG	472
cro.cro	ACTTTCTATTTCGGCTATGCTATCCTTCGCTCAATCCCCAATAAACTCGGAGG	472
sym.ree	ACTTTCTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTGGGGGG	472
bam.tho	ACTTTCTATTTCGGCTATGCTATCCTACGATCAATCCCCAACAAACTCGGAGG	472
fra.fra	ACTTTCTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTCGGAGG	472
ith.cru	ACTTTCTATTTCGGCTACGCTATCTACGCTCAATCCCCAATAAACTTGGAGG	472
ant.par	ATTTTCTATTTCGGCTATGCCATCCTACGTTCAATCCCCAACAAACTAGGAGG	472
ant.vir	ATTTTCTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAAACTAGGAGG	472
gru.ant.ant	ACTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAAACTAGGAGG	472
gru.ant.gil	ACTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAAACTAGGAGG	472
gru.ant.sha	ACTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAAACTAGGAGG	472
gru.leu	ACTTTCTATTTCGCATACGCCATCCGACGTTCAATCCCCAACAAACTAGGAGG	472
gru.can.pra	ACTTTTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
gru.can.row	ACTTTTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
gru.can.tab	ACTTTTTATTTCGGCTACTCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
gru.can.can	ACTTTTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
gru.ame	ACTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAAACTAGGAGG	472
gru.gru	ACTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAAACTAGGAGG	472
gru.mon	ACTTTTCTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAAACTAGGAGG	472
gru.nig	ACTTTCTATTTCGCATACGCTATCTGCGTTCAATCCCCAACAAACTAGGAGG	472
gru.jap	ACTTTCTATTTCGCATACGCTATCTGCGTTCAATCCCCAACAAACTAGGAGG	472
cic.boy	ACTTTCTATTTCGCATACGCCATCCTACGCTCCATCCCCAACAAACTAGGAGG	472
rhe.ame	ATTTTCTATTTCGCATATGCCATCCTACGCTCAATCCCCAATAAACTAGGAGG	472
ant.alb	ACTTTCTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
fal.fam	ACTTTCTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
fal.ver	ACTTTCTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
fal.per	ACTTTCTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
fal.spa	ACTTTCTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAAACTAGGAGG	472
ayt.ame	ATTTTTTATTTCGCATACGCTATCTGCGATCAATCCCCAACAAACTAGGAGG	472
smi.sha	ACTTTCTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAAACTAGGAGG	472
vid.cha	ACTTTCTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAAACTAGGAGG	472
chry.pic	ACTTTCTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAAACTAGGAGG	472
emy.orb.kur	ACTTTCTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAAACTAGGAGG	472
che.mud	ACTTTCTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAAACTAGGAGG	472
eum.egr.	ACTTTCTATTTCGGCTACGCCATCCTACGCTCTATCCCCAACAAACTAGGAGG	472
PRIMER 'mcb869'	CGATCAATCCCTAACAAACTAGGAGG	

... ..

Results for RID 984593689-1224-27770



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770

Query=

(328 letters)

Database: Sequences from complete mitochondrial genomes  
129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

Taxonomy reportsDistribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

(bits) Value

ref NC_001700.1	Felis catus mitochondrion, complete genome	365	e-101
ref NC_001325.1	Phoca vitulina mitochondrion, complete genome	198	1e-51
ref NC_002008.1	Canis familiaris mitochondrion, complete g...	190	4e-49
ref NC_001602.1	Halichoerus grypus mitochondrion, complete...	180	3e-46
ref NC_000884.1	Cavia porcellus complete mitochondrial genome	176	5e-45
ref NC_001808.1	Ceratotherium simum mitochondrion, complet...	165	2e-41
ref NC_001892.1	Myoxus glis mitochondrion, complete genome	153	8e-38
ref NC_001788.1	Equus asinus mitochondrion, complete genome	151	3e-37
ref NC_002073.1	Orycteropus afer complete mitochondrial ge...	149	1e-36
ref NC_001821.1	Dasyurus novemcinctus mitochondrion, comple...	141	3e-34
ref NC_001779.1	R.unicornis complete mitochondrial genome	135	2e-32
ref NC_001569.1	Mus musculus mitochondrion, complete genome	133	7e-32
ref NC_000889.1	Hippopotamus amphibius mitochondrion, comp...	125	2e-29
ref NC_001640.1	Equus caballus mitochondrion, complete genome	125	2e-29
ref NC_001794.1	Macropus robustus mitochondrion, complete ...	123	7e-29
ref NC_000845.1	Sus scrofa mitochondrion, complete genome	121	3e-28
ref NC_001665.1	Rattus norvegicus mitochondrial genome	121	3e-28
ref NC_001567.1	Bos taurus mitochondrion, complete genome	121	3e-28
ref NC_001643.1	Pan troglodytes mitochondrion, complete ge...	117	4e-27
ref NC_001941.1	Ovis aries mitochondrion, complete genome	109	1e-24
ref NC_002391.1	Talpa europaea mitochondrion, complete genome	103	7e-23
ref NC_001913.1	Oryctolagus cuniculus mitochondrion, compl...	103	7e-23
ref NC_001644.1	Pan paniscus mitochondrion, complete genome	101	3e-22
ref NC_001807.2	Human mitochondrion, complete genome	99	4e-21
ref NC_001601.1	Balaenoptera musculus mitochondrion, compl...	98	4e-21
ref NC_002009.1	Artibeus jamaicensis mitochondrion, comple...	96	2e-20
ref NC_001645.1	Gorilla gorilla mitochondrion, complete ge...	92	2e-19
ref NC_001321.1	Balaenoptera physalus mitochondrion, compl...	90	1e-18
ref NC_001610.1	Didelphis virginiana mitochondrion, comple...	80	9e-16
ref NC_002082.1	Hylobates lar mitochondrion, complete genome	70	9e-13
ref NC_001727.1	Crossostoma lacustre mitochondrion, comple...	70	9e-13
ref NC_001804.1	Latimeria chalumnae mitochondrion, complet...	68	4e-12
ref NC_000880.1	Vidua chalybeata mitochondrion, complete g...	66	1e-11
ref NC_002069.1	Corvus frugilegus mitochondrion, complete ...	64	6e-11
ref NC_000886.1	Chelonia mydas mitochondrial DNA, complete...	62	2e-10
ref NC_001646.1	Pongo pygmaeus mitochondrion, complete genome	62	2e-10
ref NC_001606.1	Cyprinus carpio mitochondrion, complete ge...	62	2e-10
ref NC_000890.1	Mustelus manazo mitochondrion, complete ge...	60	9e-10
ref NC_001323.1	Gallus gallus mitochondrion, complete genome	58	9e-10
ref NC_002079.1	Carassius auratus mitochondrion, complete ...	58	3e-09
ref NC_000934.1	Loxodonta africana mitochondrion, complete...	56	1e-08
ref NC_000878.1	Falco peregrinus mitochondrion, complete g...	56	1e-08
ref NC_000846.1	Rhea americana mitochondrion, complete genome	56	1e-08
ref NC_002196.1	Ciconia boyciana mitochondrion, complete g...	54	5e-08
ref NC_001960.1	Salmo salar mitochondrion, complete genome	54	5e-08
ref NC_001778.1	Polypterus ornatipinnis mitochondrion, com...	54	5e-08
ref NC_002083.1	Pongo pygmaeus abelii mitochondrion, compl...	52	2e-07
ref NC_001953.1	Struthio camelus complete mitochondrial ge...	52	2e-07
ref NC_001947.1	Pelomedusa subrufa mitochondrion, complete...	52	2e-07
ref NC_001770.1	Arbacia lixula mitochondrion, complete genome	52	2e-07

## Alignments

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NC_001325	15580	.....a..t.....t.....a..t..a.....c.....	15619
NC_002008	14673	.....c.....g.....a.....a.....a.....t	14729
NC_001602	15553	.....a..t.....t.....a..t..a..g.....c.....	15612
NC_000884	14650	.....g..g.....c.....a.....c.....c.....	14709
NC_001808	14662	.....a..t..c..t.....c..a..c.....c.....t...	14721
NC_001892	14654	.....c.....c.....c.....t..a..c.....c.....t...	14713
NC_001788	14671	.....c.....c.....c.....c.....c.....c.....t...	14710
NC_002078	14663	.....c.....t.....t.....a..a..a.....c.....	14716
NC_001821	14657	.....c.....t.....t.....a..t..a.....c.....c.....	14716
NC_001779	14664	.....a.....c.....c.....c.....c.....c.....	14723
NC_001569	14625	.....c.....g.....c.....c.....c.....c.....c.....	14684
NC_000889	14658	.....c.....c.....c.....c.....c.....c.....c.....	14717
NC_001640	14674	.....c.....a.....c.....c.....c.....c.....c.....	14711
NC_001794	14670	.....g..a.....c.....c.....c.....c.....c.....c.....	14727

NC_000845	15828	.....g.....t.....c.....c.....a.....c.....c.....c.....c.....a.....	15887
NC_001665	14610	.....a.....a.....c.....c.....c.....c.....t.....t.....	14669
NC_001567	15000	.....c.....a.....a.....t.....c.....c.....c.....t.....t.....	15059
NC_001643	14655	.....a.....gcc.....t.....c.....c.....c.....c.....t.....	14710
NC_001941	14645	.....g.....a.....c.....c.....c.....c.....c.....c.....t.....	14704
NC_002191	14671	.....t.....g.....g.....a.....c.....c.....c.....c.....t.....	14730
NC_001913	14661	.....a.....t.....t.....c.....t.....t.....c.....c.....t.....t.....	14720
NC_001644	14656	.....a.....gcc.....t.....c.....c.....c.....c.....c.....c.....	14711
NC_001807	15233	.....a.....gtc.....c.....c.....c.....a.....t.....t.....	15292
NC_001601	15096	.....c.....t.....t.....g.....t.....a.....a.....a.....c.....c.....	15155
NC_002009	14636	.....t.....t.....c.....a.....t.....c.....c.....c.....c.....t.....	14695
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NC_001321	15099	.....c.....c.....t.....t.....t.....a.....a.....a.....c.....t.....t.....t.....	15158
NC_001610	14663	.....t.....a.....c.....t.....t.....a.....a.....c.....t.....t.....t.....t.....	14722
NC_002082	14657	.....c.....a.....c.....c.....c.....a.....c.....c.....t.....c.....c.....t.....	14712
NC_001727	15764	.....g.....g.....t.....a.....t.....g.....c.....c.....c.....c.....	15823
NC_001804	14829	.....t.....t.....c.....c.....c.....a.....c.....g.....c.....c.....c.....	14888
NC_000880	15477	.....a.....c.....c.....c.....a.....a.....c.....c.....c.....c.....	15500
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NC_000886	14718	.....g.....c.....t.....a.....a.....a.....c.....c.....c.....c.....	14777
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NC_000890	14841	.....g.....t.....c.....c.....c.....t.....c.....t.....c.....t.....t.....	14900
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NC_001778	14763	.....g.....t.....t.....t.....c.....a.....a.....t.....c.....c.....a.....	14822
NC_001953	14115	.....c.....a.....t.....t.....cc.....c.....a.....c.....c.....c.....t.....	14169
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NC_002008	14730	.....c.t.c.....g.....at...a.....t..a.....a	14789
NC_001602	15613	.....a.....cg.ag.a.t...a.....a.....a.....a	15672
NC_000884	14710	..t..t.....c.....a.c.c.....cgat.....t.....c.....	14769
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NC_001892	14714	..t..t..a..c.c.t..cg...c.....t.at.....c.....a	14790
NC_001788	14731	..t..t..a..c.....a.....c.g.t.atc.....t..a.....c.....a	14776
NC_002078	14717	..t.....g.....t..cg.....tat.....t..a.....t..a.....a	14776
NC_001821	14717	.....t.a.....t.....a..a.c.t.t.....gt.....a.....a	14783
NC_001779	14724	..t.....c.c.t...ct...c.....a..c.....a.....a.....a	

[illegible]

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NC\_000880 15567 .....ac.....a.....a 15591  
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NC\_000886 14778 ... 14780  
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ag

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<u>NC 001911</u>	14961	.....	14980
<u>NC 001644</u>	1491	...c.....	1501
<u>NC 001807</u>	15533	..c.....c.....c....	15560
<u>NC 002009</u>	14936	.....c.....a....	14963
<u>NC 001645</u>	14955	.gc.....a.....c....	14974
<u>NC 001610</u>	14963	..c.....g..c.....a....	14990
<u>NC 002082</u>	14953	..c.....c.....	14972
<u>NC 001960</u>	16170	gt...t..a..t.....	16197
<u>NC 001951</u>	14416	.....c.....	14437

Database: Sequences from complete mitochondrial genomes

Posted date: Jun 28, 2000 10:56 AM

Number of letters in database: 3,164,247

Number of sequences in database: 129

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 788  
 Number of Sequences: 129  
 Number of extensions: 788  
 Number of successful extensions: 168  
 Number of sequences better than 10.0: 77  
 length of query: 328  
 length of database: 3,164,247  
 effective HSP length: 15  
 effective length of query: 313  
 effective length of database: 3,162,312  
 effective search space: 989803656  
 effective search space used: 989803656  
 T: 0  
 A: 30  
 X1: 6 (11.9 bits)  
 X2: 15 (29.7 bits)  
 S1: 12 (24.3 bits)  
 S2: 14 (28.2 bits)



Table 4



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query-

(328 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reportsDistribution of 50 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

		Score (bits)	E Value
gb AY005809.1	Panthera pardus cytochrome b gene, partial c...	603	e-170
gb AF051054.1 AF051054	Panthera tigris sumatrae isolate Su1...	527	e-147
gb AF051053.1 AF051053	Panthera tigris tigris isolate B7 mi...	527	e-147
gb AF051050.1 AF051050	Panthera tigris corbetti isolate C2 ...	476	e-132
gb AF051049.1 AF051049	Panthera tigris corbetti isolate C1 ...	476	e-132
gb AF051025.1 AF051025	Panthera tigris tigris isolate B9 cy...	450	e-127
gb AF051024.1 AF051024	Panthera tigris tigris isolate B8 cy...	450	e-127
gb AF051023.1 AF051023	Panthera tigris tigris isolate B7 cy...	450	e-127
gb AF051022.1 AF051022	Panthera tigris tigris isolate B6 cy...	450	e-127
gb AF051021.1 AF051021	Panthera tigris tigris isolate B5 cy...	450	e-127
gb AF051018.1 AF051018	Panthera tigris tigris isolate B2 cy...	450	e-127
gb AF051051.1 AF051051	Panthera tigris corbetti isolate C3 ...	452	e-125
gb AF051048.1 AF051048	Panthera tigris sumatrae isolate Su1...	452	e-125
gb AF051047.1 AF051047	Panthera tigris sumatrae isolate Su9...	452	e-125
gb AF051046.1 AF051046	Panthera tigris sumatrae isolate Su7...	452	e-125
gb AF051045.1 AF051045	Panthera tigris sumatrae isolate Su6...	452	e-125
gb AF051044.1 AF051044	Panthera tigris sumatrae isolate Su5...	452	e-125
gb AF051042.1 AF051042	Panthera tigris sumatrae isolate Su3...	452	e-125
gb AF051041.1 AF051041	Panthera tigris sumatrae isolate Su2...	452	e-125
gb AF051040.1 AF051040	Panthera tigris sumatrae isolate Su1...	452	e-125
gb AF051039.1 AF051039	Panthera tigris altaica isolate S15 ...	452	e-125
gb AF051038.1 AF051038	Panthera tigris altaica isolate S14 ...	452	e-125
gb AF051037.1 AF051037	Panthera tigris altaica isolate S13 ...	452	e-125
gb AF051036.1 AF051036	Panthera tigris altaica isolate S12 ...	452	e-125
gb AF051035.1 AF051035	Panthera tigris altaica isolate S11 ...	452	e-125
gb AF051034.1 AF051034	Panthera tigris altaica isolate S10 ...	452	e-125
gb AF051033.1 AF051033	Panthera tigris altaica isolate S8 c...	452	e-125
gb AF051032.1 AF051032	Panthera tigris altaica isolate S7 c...	452	e-125
gb AF051031.1 AF051031	Panthera tigris altaica isolate S6 c...	452	e-125
gb AF051030.1 AF051030	Panthera tigris altaica isolate S5 c...	452	e-125
gb AF051029.1 AF051029	Panthera tigris altaica isolate S4 c...	452	e-125
gb AF051028.1 AF051028	Panthera tigris altaica isolate S3 c...	452	e-125
gb AF051027.1 AF051027	Panthera tigris altaica isolate S2 c...	452	e-125
gb AF051026.1 AF051026	Panthera tigris altaica isolate S1 c...	452	e-125
gb AF051020.1 AF051020	Panthera tigris tigris isolate B4 cy...	452	e-125
gb AF051019.1 AF051019	Panthera tigris tigris isolate B3 cy...	444	e-122
gb AF051043.1 AF051043	Panthera tigris sumatrae isolate Su4...	444	e-122
emb X82301.1 M1PTCYTB	P.tigris mitochondrial cytochrome b gene	440	e-121
gb AF051052.1 AF051052	Panthera leo cytochrome b (cytb) gen...	438	e-121
emb X82300.1 M1PLCYTBG	P.leo mitochondrial cytochrome b gene	399	e-106
gb AB004238.1 AB004238	Felis catus mitochondrial DNA for c...	381	e-103
gb AB004237.1 AB004237	Felis catus mitochondrial DNA for c...	377	e-102
emb X82296.1 M1FDCTB	F.domesticus mitochondrial cytochrome...	365	1e-98
gb NC 001700.1	Felis catus mitochondrion, complete genome	365	1e-98
gb U20751.1 FCU20751	Felis catus mitochondrion, complete ge...	276	7e-72
gb AF125145.1 AF125145	Viverricula indica cytochrome b gene...	270	4e-70
gb AF125144.1 AF125144	Chrotogale owstoni cytochrome b gene...	255	7e-66
gb AF154975.1 AF154975	Martes martes specimen_voucher AF175...	256	7e-66
gb AB051237.1 AB051237	Martes martes mitochondrial cytb ge...	246	6e-63
gb AF125149.1 AF125149	Viverra zangalunga cytochrome b gene...		

## Alignments

cmpseq_0	1	tgaatctgaggaggctctctcagtagacaaagctaccccgacacgattctcttgcctctccac	60
AY005809	39	.....g.....c.....	98
AF051054	487	.....g.....c.....	546
AF051053	487	.....g.....c.....	546
AF051050	487	.....g.....c.....	546
AF051049	487	.....g.....c.....	546
AF051025	487	.....g.....c.....	546
AF051024	487	.....g.....c.....	546
AF051023	487	.....g.....c.....	546
AF051022	487	.....g.....c.....	546
AF051021	487	.....g.....c.....	546
AF051018	487	.....g.....c.....	546
AF051051	487	.....g.....c.....	546
AF051048	487	.....g.....c.....	546
AF051047	487	.....g.....c.....	546

<u>AF051046</u>	487	.....g..t.....	546
<u>AF051045</u>	487	.....g..t.....	546
<u>AF051044</u>	487	.....g..t.....	546
<u>AF051042</u>	487	.....g..t.....	546
<u>AF051041</u>	487	.....g..t.....	546
<u>AF051040</u>	487	.....g..t.....	546
<u>AF051039</u>	487	.....g..t.....	546
<u>AF051038</u>	487	.....g..t.....	546
<u>AF051037</u>	487	.....g..t.....	546
<u>AF051036</u>	487	.....g..t.....	546
<u>AF051035</u>	487	.....g..t.....	546
<u>AF051034</u>	487	.....g..t.....	546
<u>AF051033</u>	487	.....g..t.....	546
<u>AF051032</u>	487	.....g..t.....	546
<u>AF051031</u>	487	.....g..t.....	546
<u>AF051030</u>	487	.....g..t.....	546
<u>AF051029</u>	487	.....g..t.....	546
<u>AF051028</u>	487	.....g..t.....	546
<u>AF051027</u>	487	.....g..t.....	546
<u>AF051026</u>	487	.....g..t.....	546
<u>AF051020</u>	487	.....g..t.....	546
<u>AF051019</u>	487	.....g..t.....	546
<u>AF051043</u>	487	.....g..t.....	546
<u>X82301</u>	487	.....g..t.....	546
<u>AF051052</u>	487	.....c.....	546
<u>X82300</u>	490	.....c.....	546
<u>A8004238</u>	487	.....g.....c.....a.....	546
<u>A3004237</u>	487	.....g.....c.....a.....t.....	546
<u>X82296</u>	487	.....g.....c.....a.....	546
<u>NC 001700</u>	15524	.....g..g.....c.....a.....g.....	15583
<u>U20753</u>	15524	.....g..g.....c.....a.....g.....	15583
<u>AF125145</u>	357	.....t.....t.....c.....a.....c.....	416
<u>AF125144</u>	357	.....t.....g.....t.....t.....c.....a.....c.....	416
<u>AF154975</u>	487	.....g.....g.....c.....a.....g.....c.....	546
<u>A3051237</u>	487	.....g.....g.....c.....a.....g.....c.....	546
<u>AF125149</u>	357	.....g.....t.....g.....c.....t.....a.....t.....	416
<u>cmpseq_0</u>	61	ttcatccttccatttatcatcttcagctcttagcagcagtcacacccctctattccttcacgag	120
<u>AY005809</u>	99	.....c.....	158
<u>AF051054</u>	547	.....c.....c.....t.....	606
<u>AF051053</u>	547	.....c.....c.....t.....	606
<u>AF051050</u>	547	.....g.....c.....a.....	606
<u>AF051049</u>	547	.....g.....c.....a.....	606
<u>AF051025</u>	547	.....g.....g.....c.....a.....	606
<u>AF051024</u>	547	.....g.....g.....c.....a.....	606
<u>AF051023</u>	547	.....g.....g.....c.....a.....	606
<u>AF051022</u>	547	.....g.....g.....c.....a.....	606
<u>AF051021</u>	547	.....g.....g.....c.....a.....	606
<u>AF051018</u>	547	.....g.....g.....c.....a.....	606
<u>AF051051</u>	547	.....g.....g.....c.....a.....	606
<u>AF051048</u>	547	.....g.....g.....c.....a.....	606
<u>AF051047</u>	547	.....g.....g.....c.....a.....	606
<u>AF051046</u>	547	.....g.....g.....c.....a.....	606
<u>AF051045</u>	547	.....g.....g.....c.....a.....	606
<u>AF051044</u>	547	.....g.....g.....c.....a.....	606
<u>AF051042</u>	547	.....g.....g.....c.....a.....	606
<u>AF051041</u>	547	.....g.....g.....c.....a.....	606
<u>AF051040</u>	547	.....g.....g.....c.....a.....	606
<u>AF051039</u>	547	.....g.....g.....c.....a.....	606
<u>AF051038</u>	547	.....g.....g.....c.....a.....	606
<u>AF051037</u>	547	.....g.....g.....c.....a.....	606
<u>AF051016</u>	547	.....g.....g.....c.....a.....	606
<u>AF051035</u>	547	.....g.....g.....c.....a.....	606
<u>AF051034</u>	547	.....g.....g.....c.....a.....	606
<u>AF051033</u>	547	.....g.....g.....c.....a.....	606
<u>AF051032</u>	547	.....g.....g.....c.....a.....	606
<u>AF051031</u>	547	.....g.....g.....c.....a.....	606
<u>AF051030</u>	547	.....g.....g.....c.....a.....	606
<u>AF051029</u>	547	.....g.....g.....c.....a.....	606
<u>AF051028</u>	547	.....g.....g.....c.....a.....	606
<u>AF051027</u>	547	.....g.....g.....c.....a.....	606

[illegible]

AY005809	219	.....c.....	278
AF051054	667	.....c.....a.....	726
AF051053	667	.....c.....a.....	726
AF051050	667	.....c.....t.a.....ct.....a.c.....	726
AF051049	667	.....c.....t.a.....ct.....a.c.....	726
AF051025	667	.....c.....t.a.....ct.....a.c.....	726
AF051024	667	.....c.....t.a.....ct.....a.c.....	726
AF051023	667	.....c.....t.a.....ct.....a.c.....	726
AF051022	667	.....c.....t.a.....ct.....a.c.....	726
AF051021	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051018	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051051	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051048	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051047	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051046	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051045	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051044	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051042	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051041	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051040	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051039	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051038	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051037	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051036	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051035	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051034	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051033	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051032	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051031	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051030	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051029	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051028	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051027	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051026	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051020	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051019	667	.....c.....t.a.....ct.....a.c.....c.....	726
AF051043	667	.....c.....t.a.....ct.....g.....a.c.....	726
X82301	667	.....c.....t.a.....ct.....g.....a.c.....	726
AF051052	667	.....c.....t.a.....ct.....t.....t.....a.....	726
X82300	667	.....c.....c.....a.....t.....g.....ct.....a.....	726
AB004238	667	.....c.....c.....a.....t.....g.....ct.....a.....	726
AB004237	667	.....c.....c.....a.....t.....g.....ct.....a.....	726
X82296	667	.....c.....c.....a.....t.....g.....ct.....a.....	15763
NC_001700	15704	.....c.....c.....a.....t.....g.....ct.....a.....	15763
U20753	15704	.....c.....c.....a.....t.....g.....ct.....a.....	596
AF125145	537	.....c.....c.....a.....t.....g.....ct.....a.....	596
AF125144	537	.....c.....c.....a.....t.....g.....ct.....a.....	726
AF154975	667	.....c.....c.....a.....t.....g.....ct.....a.....	726
AB051237	667	.....c.....c.....a.....t.....g.....ct.....a.....	596
AF125149	537	.....c.....c.....a.....t.....g.....ct.....a.....	596
cmpseq_0	241	gccccattctccaccagacctgtcaggagaccccgataaactacatccctgccaaacccctcta	100
AY005809	279	.....c.....	338
AF051054	727	.....a.....g.....c.....	786
AF051053	727	.....a.....g.....c.....	786
AF051050	727	.....a.....c.....c.....	786
AF051049	727	.....a.....c.....c.....	786
AF051025	727	.....a.....c.....c.....	786
AF051024	727	.....a.....c.....c.....	786
AF051023	727	.....a.....c.....c.....	786
AF051022	727	.....a.....c.....c.....	786
AF051021	727	.....a.....c.....c.....	786
AF051018	727	.....a.....c.....c.....	786
AF051051	727	.....a.....c.....c.....	786
AF051048	727	.....a.....c.....c.....	786
AF051047	727	.....a.....c.....c.....	786
AF051046	727	.....a.....c.....c.....	786
AF051045	727	.....a.....c.....c.....	786
AF051044	727	.....a.....c.....c.....	786
AF051043	727	.....a.....c.....c.....	786
AF051042	727	.....a.....c.....c.....	786
AF051041	727	.....a.....c.....c.....	786
AF051040	727	.....a.....c.....c.....	786
AF051039	727	.....a.....c.....c.....	786
AF051038	727	.....a.....c.....c.....	786
AF051037	727	.....a.....c.....c.....	786
AF051036	727	.....a.....c.....c.....	786
AF051035	727	.....a.....c.....c.....	786
AF051034	727	.....a.....c.....c.....	786
AF051033	727	.....a.....c.....c.....	786
AF051032	727	.....a.....c.....c.....	786
AF051031	727	.....a.....c.....c.....	786
AF051030	727	.....a.....c.....c.....	786
AF051029	727	.....a.....c.....c.....	786
AF051028	727	.....a.....c.....c.....	786
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AF051023	727	.....a.....c.....c.....	786
AF051022	727	.....a.....c.....c.....	786
AF051021	727	.....a.....c.....c.....	786
AF051020	727	.....a.....c.....c.....	786
AF051019	727	.....a.....c.....c.....	786
AF051018	727	.....a.....c.....c.....	786
AF051017	727	.....a.....c.....c.....	786
AF051016	727	.....a.....c.....c.....	786
AF051015	727	.....a.....c.....c.....	786
AF051014	727	.....a.....c.....c.....	786
AF051013	727	.....a.....c.....c.....	786
AF051012	727	.....a.....c.....c.....	786
AF051011	727	.....a.....c.....c.....	786
AF051010	727	.....a.....c.....c.....	786
AF051009	727	.....a.....c.....c.....	786
AF051008	727	.....a.....c.....c.....	786
AF051007	727	.....a.....c.....c.....	786
AF051006	727	.....a.....c.....c.....	786
AF051005	727	.....a.....c.....c.....	786
AF051004	727	.....a.....c.....c.....	786
AF051003	727	.....a.....c.....c.....	786
AF051002	727	.....a.....c.....c.....	786
AF051001	727	.....a.....c.....c.....	786

AF053040	727	.....a.....c.....c.....c.....	786
AF053039	727	.....a.....c.....c.....c.....	786
AF053038	727	.....a.....c.....c.....c.....	786
AF053037	727	.....a.....c.....c.....c.....	786
AF053036	727	.....a.....c.....c.....c.....	786
AF053035	727	.....a.....c.....c.....c.....	786
AF053034	727	.....a.....c.....c.....c.....	786
AF053033	727	.....a.....c.....c.....c.....	786
AF053032	727	.....a.....c.....c.....c.....	786
AF053031	727	.....a.....c.....c.....c.....	786
AF053030	727	.....a.....c.....c.....c.....	786
AF053029	727	.....a.....c.....c.....c.....	786
AF053028	727	.....a.....c.....c.....c.....	786
AF053027	727	.....a.....c.....c.....c.....	786
AF053026	727	.....a.....c.....c.....c.....	786
AF053020	727	.....a.....c.....c.....c.....	786
AF053019	727	.....a.....c.....c.....c.....	786
AF053043	727	.....a.....c.....c.....c.....	786
X82301	727	.....a.....c.....c.....c.....	786
AF053052	727	.....a.....c.....c.....c.....	786
X82300	727	.....a.....c.....c.....c.....	786
A3004238	727	.....c.....c.....a..c.g.....a.....	786
A3004237	727	.....c.....c.....a..c.....a.....	786
X82296	727	.....c.....c.....a..c.....a.....	786
NC 001700	15764	.....c.....c.....a..c.....a.....	15823
U20753	15764	.....c.....c.....a..c.....a.....	15823
AF125145	597	.....c.....c.....a.....c.....c.....	656
AF125144	597	.....c.....c.....a.....c.....c.....	656
AF154975	727	.....a.....c.....c.g.....a..c.....a..c	786
A3051237	727	.....a.....c.....c.g.....a..c.....a..c	786
AF125149	597	.....c.....c.....a.....c.....c.....	656
cmpseq_0	301	aatacccccccccatatcaagcctgaat	328
AY005809	339	.....	366
AF053054	787	..c.....	808
AF053053	787	..c.....	808
AF053050	787	.....c.....c.....	814
AF053049	787	.....c.....c.....	814
AF053025	787	.....c.....c.....	814
AF053024	787	.....c.....c.....	814
AF053023	787	.....c.....c.....	814
AF053022	787	.....c.....c.....	814
AF053021	787	.....c.....c.....	814
AF053018	787	.....c.....c.....	814
AF053051	787	.....c.....c.....	814
AF053048	787	.....c.....c.....	814
AF053047	787	.....c.....c.....	814
AF053046	787	.....c.....c.....	814
AF053045	787	.....c.....c.....	814
AF053044	787	.....c.....c.....	814
AF053042	787	.....c.....c.....	814
AF053041	787	.....c.....c.....	814
AF053040	787	.....c.....c.....	814
AF053039	787	.....c.....c.....	814
AF053038	787	.....c.....c.....	814
AF053037	787	.....c.....c.....	814
AF053036	787	.....c.....c.....	814
AF053035	787	.....c.....c.....	814
AF053034	787	.....c.....c.....	814
AF053033	787	.....c.....c.....	814
AF053032	787	.....c.....c.....	814
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AF053030	787	.....c.....c.....	814
AF053029	787	.....c.....c.....	814
AF053028	787	.....c.....c.....	814
AF053027	787	.....c.....c.....	814
AF053026	787	.....c.....c.....	814
AF053020	787	.....c.....c.....	814
AF053012	787	.....c.....c.....	814
AF053043	787	.....c.....c.....	814
X82301	787	.....c.....c.....	814

<u>AF051052</u>	787	.gc.....a.....	812
<u>X82100</u>	787	.gc.....a.....	814
<u>AB004238</u>	787	.....c..a.....	814
<u>AB004237</u>	787	.....c..a.....	814
<u>X82296</u>	787	.....c..a.....	814
<u>NC 001700</u>	15824	.....c..a.....	15851
<u>U20753</u>	15824	.....c..a.....	15851
<u>AF125144</u>	657	..c.....	664
<u>AF154975</u>	787	..c..a..a.....	803
<u>AB051237</u>	787	..c..a..a.....	803
<u>AF125149</u>	657	..c.....	664

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,861,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 460542

Number of Sequences: 807597

Number of extensions: 460542

Number of successful extensions: 22671

Number of sequences better than 10.0: 6487

length of query: 328

length of database: 2,861,827,885

effective HSP length: 20

effective length of query: 308

effective length of database: 2,847,675,945

effective search space: 877084191060

effective search space used: 877084191060

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 19 (38.2 bits)

**Table 5.** Reference animals and the allocated code numbers included in the study

<b>SN.</b>	<b>Code number</b>	<b>Name of the animal</b>	<b>Zoological name</b>
1	bhz25t	Indian tiger	<i>Panthera tigris tigris</i>
2	bhz26t	Indian tiger	<i>Panthera tigris tigris</i>
3	bhz30t	Indian tiger	<i>Panthera tigris tigris</i>
4	bhz45t	Indian tiger	<i>Panthera tigris tigris</i>
5	bhz56t	Indian tiger	<i>Panthera tigris tigris</i>
6	bhz63t	Indian tiger	<i>Panthera tigris tigris</i>
7	bhz20wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
8	bhz22wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
9	bhz23wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
10	bhz28wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
11	gz1l	Normal leopard	<i>Panthera pardus</i>
12	gz2l	Normal leopard	<i>Panthera pardus</i>
13	gz3l	Normal leopard	<i>Panthera pardus</i>
14	gz21cl	Clouded leopard	<i>Neofelis nebulosa</i>
15	gz22cl	Clouded leopard	<i>Neofelis nebulosa</i>
16	darz14sl	Snow leopard	<i>Panthera uncia</i>
17	darz15sl	Snow leopard	<i>Panthera uncia</i>
18	darz16sl	Snow leopard	<i>Panthera uncia</i>
19	sbz22al	Asiatic lion	<i>Panthera leo persica</i>
20	sbz38al	Asiatic lion	<i>Panthera leo persica</i>
21	sbz39al	Asiatic lion	<i>Panthera leo persica</i>
22	humsk	Human	<i>Homo sapiens sapiens</i>
23	chimss	Chimpanzee	<i>Pan sp.</i>



Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

sbz22al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	50
sbz38al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
sbz39al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
adil.flesh	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCCTGACACGATTCTTTGCCTTCCAC	60
gz1nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCCTGACACGATTCTTTGCCTTCCAC	60
gz2nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCCTGACACGATTCTTTGCCTTCCAC	60
gz3nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCCTGACACGATTCTTTGCCTTCCAC	60
bhz23wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz28wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz22wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz20wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz63t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz56t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz26t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz30t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz45t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz25t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
d=14sl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
d=15sl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
d=16sl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
gz21cl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
gz22cl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
chimss	TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTACCCCTTACACGATTCTTCACCTTCCAC	60
humsk	TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCCTCACACGATTCTTTACCTTCCAC	60
*****		
sbz22al	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
sbz38al	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
sbz39al	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
adil.flesh	TTTCATCCTTCCATTATTCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
gz1nl	TTTCATCCTTCCATTATTCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
gz2nl	TTTCATCCTTCCATTATTCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
gz3nl	TTTCATCCTTCCATTATTCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz23wt	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz28wt	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz22wt	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz20wt	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz63t	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz56t	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz26t	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz30t	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz45t	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
bhz25t	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
d=14sl	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
d=15sl	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
d=16sl	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
gz21cl	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
gz22cl	TTTCATCCTTCCATTATTCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG	120
chimss	TTTATCTTACCCTTCAATTACACAGCCCTAACCAACCTTCATCTCTCTATTCTTACACGAA	120
humsk	TTTCATCTTGCCTTCAATTATTCAGCCCTAGCAGCAGTCCACCTCCTATTCTTGCACGAA	120
.. .. .		
sbz22al	ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAA TTCCATTCCATCCA	190
sbz38al	ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAA TTCCATTCCATCCA	190

sbz39a1 ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAATTCCATTCCATCCA 130  
adil.flesh ACAGGATCTAACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCATTCCACCCA 130  
g=1n1 ACAGGATCTAACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCATTCCACCCA 130  
g=2n1 ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
g=3n1 ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=23wt ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=28wt ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=22wt ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=20wt ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=63t ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=56t ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=26t ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=30t ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=45t ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
bh=25t ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
d=14s1 ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
d=15s1 ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
d=16s1 ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130  
g=21c1 ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCCAGACAAAATTCATTCCACCCA 130  
g=22c1 ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCCAGACAAAATTCATTCCACCCA 130  
chimss ACAGGATCAAATAACCCCTCGGGAATCACCTCCCCTCCGACAAAATTCATTCCACCCA 130  
humsk ACGGGATCAAACAACCCCTAGGAATCACCTCCCCTCCGATAAAAATTCATTCCACCCA 130  
\* \* \* \* \*

sbz22a1 TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
sbz38a1 TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
sbz39a1 TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
adil.flesh TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
g=1n1 TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
g=2n1 TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
g=3n1 TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=23wt TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=28wt TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=22wt TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=20wt TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=63t TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=56t TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=26t TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=30t TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=45t TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
bh=25t TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
d=14s1 TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
d=15s1 TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
d=16s1 TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
g=21c1 TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
g=22c1 TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
chimss TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
humsk TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240  
\* \* \* \* \*

sbz22a1 GTCCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300  
sbz38a1 GTCCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300  
sbz39a1 GTCCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300  
adil.flesh GTCCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300  
g=1n1 GTCCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300  
g=2n1 GTCCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300  
g=3n1 GTCCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300  
bh=23wt GTCCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300

bhz28wt GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
bhz22wt GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
bhz20wt GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
bhz63t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
bhz56t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
bhz26t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
bhz30t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
bhz45t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
bhz25t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
dz14sl GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
dz15sl GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
dz16sl GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATACTACATCCCCGCCAACCCCTCTA 300  
gz21cl GTTCTATTCTCCCCAGACCTACTAGGAGACCCGTGACAAATTACACTCCCCGCCAACCCCTCTA 300  
gz22cl GTTCTATTCTCCCCAGACCTACTAGGAGACCCGTGACAAATTACACTCCCCGCCAACCCCTCTA 300  
chimss AACTATTCTCACCAGACCTCTAGGGCGATCCAGACAATAACCTAGCTAACCCCTTA 300  
humsk AACTATTCTCACCAGACCTCTAGGGCGATCCAGACAATAACCTAGCTAACCCCTTA 300

\*\*\*\*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

sbz22al AGCACCCCTCCCCATATCAAACCTGAAT 328  
sbz38al AGCACCCCTCCCCATATCAAACCTGAAT 328  
sbz39al AGCACCCCTCCCCATATCAAACCTGAAT 328  
adil.flesh AATACCCCTCCCCATATCAAGCCTGAAT 328  
gz1nl AATACCCCTCCCCATATCAAGCCTGAAT 328  
gz2nl AATACCCCTCCCCATATCAAGCCTGAAT 328  
gz3nl AATACCCCTCCCCATATCAAGCCTGAAT 328  
bhz23wt AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz28wt AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz22wt AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz20wt AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz63t AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz56t AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz26t AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz30t AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz45t AACACCCCTCCCCATATCAAGCGCGAAT 328  
bhz25t AACACCCCTCCCCATATCAAGCGCGAAT 328  
dz14sl AACACCCCTCCCCATATCAAGCCCGAAT 328  
dz15sl AACACCCCTCCCCATATCAAGCCCGAAT 328  
dz16sl AACACCCCTCCCCATATCAAGCCCGAAT 328  
gz21cl AATACCCCTCCCCATATCAAGCCTGAAT 328  
gz22cl AATACCCCTCCCCATATCAAGCCTGAAT 328  
chimss AACACCCCACCCCACATTAAACCCGAAT 328  
humsk AACACCCCTCCCCACATCAAGCCCGAAT 328

\* \* \* \* \*







Table 7d

Position	273	276	279	282	284	285	287	288	291	294	297	298	302	303	309	315	318	321	323	324
adll.flesh	C	T	C	C	T	C	C	T	C	C	T	C	A	T	T	T	C	G	C	T
gz1l	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
gz2l	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	.
gz3l	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	.
bhz25t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz26t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz30t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz45t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz56t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz20wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz22wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz23wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
dz14sl	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	.	C
dz15sl	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	.	C
sbz22al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	.	A	.	.
sbz38al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	.	A	.	.
gz21cl	T	C	T	.	C	T	.	C	.	.	.	.	.	.	.	.	.	.	.	.
gz22cl	T	C	T	.	C	T	.	C	.	.	.	.	.	.	.	.	.	.	.	.
chlmss	A	C	A	T	C	A	T	A	T	C	T	C	A	C	A	C	A	T	C	A
humsk	A	C	A	T	C	A	T	A	T	C	T	C	A	C	A	C	A	T	C	A

Table 8. Percent similarity matrix calculated by pair-wise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

	bhz20wt	bhz25t	dz14sl	humsk	chlmss	sbz22al	gz1L	gz2L	gz3L	gz21cl	adil.flesh
bhz20wt		100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
bhz25t	100		99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
dz14sl	99.1	99.1		81.4	78.4	93	94.8	95.1	95.1	89.3	95.1
humsk	81.7	81.7	81.4		86.9	79.6	81.1	80.2	80.2	79	81.4
chlmss	78.7	78.7	78.4	86.9		78.7	79.6	78.7	78.7	76.8	79.9
sbz22al	93.3	93.3	93	79.6	78.7		92.1	92.4	92.4	89	92.4
gz1L	95.1	95.1	94.8	81.1	79.6	92.1		98.5	98.5	89.3	99.7
gz2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5		100	88.1	98.2
gz3L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	100		88.1	98.2
gz21cl	89.6	89.6	89.3	79	76.8	89	89.3	88.1	88.1		89.6
adil.flesh	95.4	95.4	95.1	81.4	79.9	92.4	99.7	98.2	98.2	89.6	



## Table 10



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,  
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997).  
"Gapped BLAST and PSI-BLAST: a new generation of protein database search  
programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query=

(25 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search  
please refer to the BLAST FAQs

Taxonomy reportsDistribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

	Score	E
	(bits)	Value
gb AF231651.1 AF231651 Strongylura notata clone HB-82 cyto...	50	2e-05
gb AF231650.1 AF231650 Strongylura notata clone HB-159 cyto...	50	2e-05
ref NC_002672.1  Dinornis giganteus mitochondrion, complete...	50	2e-05
ref NC_002673.1  Emeus crassus mitochondrion, complete genome	50	2e-05
gb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome...	50	2e-05
gb AF232013.1 AF232013 Bradypus variegatus cytochrome b gen...	50	2e-05
gb AY016015.1  Emeus crassus mitochondrion, complete genome	50	2e-05
gb AY016013.1  Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb AY016014.1  Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb AF230167.1 AF230167 Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb AF074594.1 AF074594 Baeolophus bicolor cytochrome b gene...	50	2e-05
gb AY005210.1  Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb AY005209.1  Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb AY005208.1  Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb AY005205.1  Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb AY005204.1  Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb AY005203.1  Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb AY005201.1  Poospiza boliviana cytochrome b (cytb) gene...	50	2e-05
gb AY005199.1  Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb AY005198.1  Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb AF155870.1 AF155870 Heterocephalus glaber cytochrome b (...)	50	2e-05
gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome...	50	2e-05
gb AF102095.1 AF102095S1 Corythaixoides concolor cytochrome...	50	2e-05
gb AF271065.1 AF271065 Mustela erminea specimen-voucher AF1...	50	2e-05
gb AF243857.1 AF243857 Strongylura notata notata cytochrome...	50	2e-05
gb AF243856.1 AF243856 Strongylura notata forsythia cytochr...	50	2e-05
ref NC_001567.1  Bos taurus mitochondrion, complete genome	50	2e-05
gb AF306872.1 AF306872 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306871.1 AF306871 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306870.1 AF306870 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306868.1 AF306868 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF010406.1 AF010406 Ovis aries complete mitochondrial ge...	50	2e-05
gb AF248662.1 AF248662 Gryllus campestris haplotype 2 cyto...	50	2e-05
gb AF248661.1 AF248661 Gryllus campestris haplotype 1 cyto...	50	2e-05
gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge...	50	2e-05
gb AF283644.1 AF283644 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283643.1 AF283643 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283642.1 AF283642 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283641.1 AF283641 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283637.1 AF283637 Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05
gb AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb AF283634.1 AF283634 Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb AF283633.1 AF283633 Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb AF283630.1 AF283630 Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb AF283629.1 AF283629 Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb AF283627.1 AF283627 Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
gb AF283626.1 AF283626 Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
gb AF283625.1 AF283625 Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb AF283623.1 AF283623 Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
gb AF283622.1 AF283622 Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb AF283621.1 AF283621 Elaphe obsoleta LSUMZ 39925 cytochro...	50	2e-05
gb AF283620.1 AF283620 Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05
gb AF283619.1 AF283619 Elaphe obsoleta LSUMZ 39162 cytochrom...	50	2e-05
gb AF283618.1 AF283618 Elaphe obsoleta LSUMZ H15896 cytoch...	50	2e-05
gb AF283617.1 AF283617 Elaphe obsoleta LSUMZ H15892 cytoch...	50	2e-05
gb AF283616.1 AF283616 Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05
gb AF283615.1 AF283615 Elaphe obsoleta LSUMZ H15890 cytoch...	50	2e-05
gb AF283614.1 AF283614 Elaphe obsoleta LSUMZ H15887 cytoch...	50	2e-05
gb AF283613.1 AF283613 Elaphe obsoleta LSUMZ H15884 cytoch...	50	2e-05

**Table 9.** Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

<b>SL.</b>	<b>Name</b>	<b>P, S/AFF</b>	<b>P, S/AFR</b>
1	Indian black buck ( <i>Antelope cervicapra</i> )	97, 58	96, 54
2	Sheep ( <i>Ovis</i>	87, 53	96, 54
3	Pig ( <i>Sus scrofa</i> )	87, 52	87, 41
4	Fresh water dolphin ( <i>Platanista gangetica</i> )	86, 49	82, 47

## Sequences producing significant alignments:

	Score	E
	(bits)	Value
gb AF231651.1 AF231651 Strongylura notata clone HB-82 cytoc...	50	2e-05
gb AF231650.1 AF231650 Strongylura notata clone HB-159 cyto...	50	2e-05
ref NC_002672.1  Dinornis giganteus mitochondrion, complete...	50	2e-05
ref NC_002673.1  Emeus crassus mitochondrion, complete genome	50	2e-05
gb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome...	50	2e-05
gb AF232013.1 AF232013 Bradypus variegatus cytochrome b gen...	50	2e-05
gb AY016015.1  Emeus crassus mitochondrion, complete genome	50	2e-05
gb AY016013.1  Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb AY016014.1  Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb AF230167.1 AF230167 Bonasa umbellus cytochrome b (CYT3) ...	50	2e-05
gb AF074594.1 AF074594 Baeolophus bicolor cytochrome b gene...	50	2e-05
gb AY005210.1  Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb AY005209.1  Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb AY005208.1  Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb AY005205.1  Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb AY005204.1  Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb AY005203.1  Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb AY005201.1  Poospiza boliviana cytochrome b (cytb) gene,...	50	2e-05
gb AY005199.1  Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb AY005198.1  Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb AF155870.1 AF155870 Heterocephalus glaber cytochrome b (...)	50	2e-05
gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome...	50	2e-05
gb AF102095.1 AF102095S1 Corythaixoides concolor cytochrome...	50	2e-05
gb AF271065.1 AF271065 Mustela erminea specimen-voucher AF1...	50	2e-05
gb AF243857.1 AF243857 Strongylura notata notata cytochrome...	50	2e-05
gb AF243856.1 AF243856 Strongylura notata forsythia cytochr...	50	2e-05
ref NC_001567.1  Bos taurus mitochondrion, complete genome	50	2e-05
gb AF306872.1 AF306872 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306871.1 AF306871 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306870.1 AF306870 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306868.1 AF306868 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF010406.1 AF010406 Ovis aries complete mitochondrial ge...	50	2e-05
gb AF248662.1 AF248662 Gryllus campestris haplotype 2 cytoc...	50	2e-05
gb AF248661.1 AF248661 Gryllus campestris haplotype 1 cytoc...	50	2e-05
gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge...	50	2e-05
gb AF283644.1 AF283644 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283643.1 AF283643 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283642.1 AF283642 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283641.1 AF283641 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283637.1 AF283637 Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05
gb AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb AF283634.1 AF283634 Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb AF283633.1 AF283633 Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb AF283630.1 AF283630 Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb AF283629.1 AF283629 Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb AF283627.1 AF283627 Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
gb AF283626.1 AF283626 Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
gb AF283625.1 AF283625 Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb AF283623.1 AF283623 Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
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gb AF283621.1 AF283621 Elaphe obsoleta LSUMZ 37225 cytochro...	50	2e-05
gb AF283620.1 AF283620 Elaphe obsoleta LSUMZ 37163 cytochro...	50	2e-05
gb AF283619.1 AF283619 Elaphe obsoleta LSUMZ 37162 cytochrom...	50	2e-05
gb AF283618.1 AF283618 Elaphe obsoleta LSUMZ H15896 cytochr...	50	2e-05
gb AF283617.1 AF283617 Elaphe obsoleta LSUMZ H15892 cytochr...	50	2e-05
gb AF283616.1 AF283616 Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05
gb AF283615.1 AF283615 Elaphe obsoleta LSUMZ H15890 cytochr...	50	2e-05
gb AF283614.1 AF283614 Elaphe obsoleta LSUMZ H15889 cytochr...	50	2e-05
gb AF283613.1 AF283613 Elaphe obsoleta LSUMZ H15888 cytochr...	50	2e-05

gb AF283612.1 AF283612	Elaphe obsoleta LSUMZ H15884 cytochr...	50	2e-05
gb AF283611.1 AF283611	Elaphe obsoleta LSUMZ H15031 cytochr...	50	2e-05
gb AF283610.1 AF283610	Elaphe obsoleta LSUMZ H15030 cytochr...	50	2e-05
gb AF283609.1 AF283609	Elaphe obsoleta CAS 169468 cytochrom...	50	2e-05
gb AF283608.1 AF283608	Elaphe obsoleta LSUMZ H14782 cytochr...	50	2e-05
gb AF283607.1 AF283607	Elaphe obsoleta LSUMZ H14781 cytochr...	50	2e-05
gb AF283606.1 AF283606	Elaphe obsoleta LSUMZ H14724 cytochr...	50	2e-05
gb AF283605.1 AF283605	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283604.1 AF283604	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283603.1 AF283603	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283602.1 AF283602	Elaphe obsoleta LSUMZ H3388 cytochro...	50	2e-05
gb AF283601.1 AF283601	Elaphe obsoleta LSUMZ H3385 cytochro...	50	2e-05
gb AF283600.1 AF283600	Elaphe obsoleta LSUMZ H3384 cytochro...	50	2e-05
gb AF283599.1 AF283599	Elaphe bairdi LSUMZ H3382 cytochrome...	50	2e-05
gb AF283598.1 AF283598	Elaphe bairdi LSUMZ H3381 cytochrome...	50	2e-05
gb AF283597.1 AF283597	Elaphe obsoleta LSUMZ H3379 cytochro...	50	2e-05
gb AF283596.1 AF283596	Elaphe obsoleta LSUMZ 39616 cytochro...	50	2e-05
gb AF283595.1 AF283595	Elaphe obsoleta LSUMZ H3376 cytochro...	50	2e-05
gb AF283594.1 AF283594	Elaphe obsoleta LSUMZ H3345 cytochro...	50	2e-05
gb AF283593.1 AF283593	Elaphe obsoleta LSUMZ H3309 cytochro...	50	2e-05
gb AF283592.1 AF283592	Elaphe obsoleta LSUMZ H3306 cytochro...	50	2e-05
gb AF283591.1 AF283591	Elaphe obsoleta LSUMZ H3276 cytochro...	50	2e-05
gb AF283590.1 AF283590	Elaphe obsoleta LSUMZ H3246 cytochro...	50	2e-05
gb AF283589.1 AF283589	Elaphe obsoleta LSUMZ H3212 cytochro...	50	2e-05
gb AF283588.1 AF283588	Elaphe obsoleta LSUMZ H3209 cytochro...	50	2e-05
gb AF283587.1 AF283587	Elaphe obsoleta LSUMZ H3206 cytochro...	50	2e-05
gb AF283586.1 AF283586	Elaphe obsoleta LSUMZ H3191 cytochro...	50	2e-05
gb AF283585.1 AF283585	Elaphe obsoleta LSUMZ H3190 cytochro...	50	2e-05
gb AF283584.1 AF283584	Elaphe obsoleta LSUMZ H3189 cytochro...	50	2e-05
gb AF283583.1 AF283583	Elaphe obsoleta LSUMZ H3188 cytochro...	50	2e-05
gb AF283582.1 AF283582	Elaphe obsoleta LSUMZ H3186 cytochro...	50	2e-05
gb AF283581.1 AF283581	Elaphe obsoleta LSUMZ H3169 cytochro...	50	2e-05
gb AF283580.1 AF283580	Elaphe obsoleta CAS 203083 cytochrom...	50	2e-05
gb AF283579.1 AF283579	Elaphe obsoleta CAS 203079 cytochrom...	50	2e-05
gb AF283578.1 AF283578	Elaphe obsoleta LSUMZ H2286 cytochro...	50	2e-05
gb AF283577.1 AF283577	Elaphe obsoleta CAS 208631 cytochrom...	50	2e-05
gb AF283576.1 AF283576	Elaphe obsoleta LSUMZ H2229 cytochro...	50	2e-05
gb AF187030.1 AF187030	Rhinophylla pumilio isolate TK46001 ...	50	2e-05
gb AF310052.1 AF310052	Poospiza hispaniolensis cytochrome b...	50	2e-05
gb AF310046.1 AF310046	Volatinia jacarina cytochrome b gene...	50	2e-05
gb AF171919.1 AF171919	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF171897.1 AF171897	Trimeresurus mucrosquamatus cytb gen...	50	2e-05
gb AF290174.1 AF290174	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb AF290173.1 AF290173	Agelaius phoeniceus cytochrome b (cy...	50	2e-05
gb AF290171.1 AF290171	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF290170.1 AF290170	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF290150.1 AF290150	Volatinia jacarina cytochrome b (cyt...	50	2e-05
gb AF176252.1 AF176252	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb AF176251.1 AF176251	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb AF163907.1 AF163907	Microtus xanthognathus cytochrome b ...	50	2e-05
gb AF163904.1 AF163904	Microtus pinetorum cytochrome b gene...	50	2e-05
gb AF163901.1 AF163901	Microtus ochrogaster cytochrome b ge...	50	2e-05
gb AF163899.1 AF163899	Microtus miurus cytochrome b gene, c...	50	2e-05
gb AF163891.1 AF163891	Microtus californicus cytochrome B (...)	50	2e-05
gb AF163890.1 AF163890	Microtus abbreviatus cytochrome B (c...	50	2e-05
gb AF288524.1 AF288524	Dipsochelys dussumieri isolate Germa...	50	2e-05
gb AF288523.1 AF288523	Dipsochelys dussumieri isolate white...	50	2e-05
gb AF288522.1 AF288522	Dipsochelys dussumieri isolate Aldy ...	50	2e-05
gb AF123530.1 AF123530	Psilopogon pyrolophus cytochrome b (...)	50	2e-05
gb AF123512.1 AF123512	Eubucco bourcierii tucinkae cytochro...	50	2e-05
gb AF206548.1 AF206548	Adolfus vauereselli cytochrome b gen...	50	2e-05
gb AF197867.1 AF197867	Gymnorhina tibicen cytochrome b gene...	50	2e-05
gb U63397.2 SEU63397	Sitta europaea cytochrome b gene, part...	50	2e-05
ref NC 001945.1	Dinodon semicarinatus mitochondrion, compl...	50	2e-05
ref NC 001831.1	Dasypus novemcinctus mitochondrion, comple...	50	2e-05
gb AF141217.1 AF141217	Dasymys incomtus country Tanzania cy...	50	2e-05
gb AF201615.1 AF201615	Pantodon buchholzi cytochrome b gene...	50	2e-05
gb AF077920.1 AF077920	Bombus nevadensis cytochrome b gene...	50	2e-05
gb AF190612.1 AF190612	Oreamnos americanus cytochrome b (cy...	50	2e-05
gb J01124.1 BQVMT	Bos taurus mitochondrion, complete genome	50	2e-05
gb AF191810.1 AF191810	Cochlearius cochlearius cytochrome b...	50	2e-05

gb U89161.1 CAU89161	Chlorostilbon aureoventris cytochrome ...	50	2e-05
gb U89171.1 AFU89171	Asio flammeus cytochrome b (cytb) gene...	50	2e-05
gb AF217811.1 AF217811	Homoroselaps lacteus cytochrome b ge...	50	2e-05
gb AF217822.1 AF217822	Hydrophis semperi cytochrome b gene...	50	2e-05
gb AF217813.1 AF217813	Acanthophis antarcticus cytochrome b...	50	2e-05
gb AF220406.1 AF220406	Calliophis kelloggi cytochrome b (cy...	50	2e-05
gb AF126430.1 AF126430	Ellobius fuscocapillus cytochrome b ...	50	2e-05
gb AF090337.1 AF090337	Aythya americana mitochondrion, comp...	50	2e-05
gb AF059111.1 AF059111	Sarkidiornis melanotos cytochrome b ...	50	2e-05
gb AF059053.1 AF059053	Aix sponsa cytochrome b gene, partia...	50	2e-05
gb AF099308.1 AF099308	Icterus wagleri wagleri cytochrome b...	50	2e-05
gb AF099295.1 AF099295	Icterus gularis yucatanensis cytochr...	50	2e-05
gb AF099294.1 AF099294	Icterus gularis tamaulipensis cytoch...	50	2e-05
gb AF099293.1 AF099293	Icterus gularis gularis cytochrome b...	50	2e-05
gb AF160610.1 AF160610	Cricetomys emini Cemi636 cytochrome ...	50	2e-05
gb AF036280.1 AF036280	Tragelaphus strepsiceros cytochrome ...	50	2e-05
gb AF036277.1 AF036277	Tragelaphus scriptus cytochrome b (c...	50	2e-05
gb AF036274.1 AF036274	Tetracerus quadricornis cytochrome b (cytb) ...	50	2e-05
gb AF194218.1 AF194218	Phrynosoma platyrhinos cytochrome b ...	50	2e-05
gb AF194216.1 AF194216	Urosaurus ornatus cytochrome b gene...	50	2e-05
ref NC_002009.1 NC_002009	Artibeus jamaicensis mitochondrion, comple...	50	2e-05
ref NC_001941.1 NC_001941	Ovis aries mitochondrion, complete genome	50	2e-05
ref NC_000877.1 NC_000877	Aythya americana mitochondrion, complete g...	50	2e-05
ref NC_000846.1 NC_000846	Rhea americana mitochondrion, complete genome	50	2e-05
gb U27551.1 GCU27551	Grus canadensis tabida cytochrome b (c...	50	2e-05
gb AF089058.1 AF089058	Quiscalus quiscula cytochrome b (cyt...	50	2e-05
gb AF089055.1 AF089055	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF089054.1 AF089054	Quiscalus lugubris cytochrome b (cyt...	50	2e-05
gb AF089046.1 AF089046	Oreopsar bolivianus cytochrome b (cy...	50	2e-05
gb AF089042.1 AF089042	Molothrus badius cytochrome b (cytb)...	50	2e-05
gb AF089039.1 AF089039	Macroagelaius imthurni cytochrome b ...	50	2e-05
gb AF089037.1 AF089037	Lamprosarpis tanagra cytochrome b (...)	50	2e-05
gb AF089026.1 AF089026	Gymnomystax mexicanus cytochrome b (...)	50	2e-05
gb AF089025.1 AF089025	Gnorimopsar chopi cytochrome b (cytb...	50	2e-05
gb AF089024.1 AF089024	Euphagus cyanocephalus cytochrome b ...	50	2e-05
gb AF089023.1 AF089023	Euphagus carolinus cytochrome b (cyt...	50	2e-05
gb AF089021.1 AF089021	Dives wartszewiczi cytochrome b (cyt...	50	2e-05
gb AF089020.1 AF089020	Curaeus curaeus cytochrome b (cytb) ...	50	2e-05
gb AF089016.1 AF089016	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF089013.1 AF089013	Agelaius xanthophthalmus cytochrome ...	50	2e-05
gb AF089012.1 AF089012	Agelaius xanthopus cytochrome b (cyt...	50	2e-05
gb AF089008.1 AF089008	Agelaius phoeniceus sub-species phoe...	50	2e-05
gb AF089006.1 AF089006	Agelaius humeralis cytochrome b (cyt...	50	2e-05
gb AF089005.1 AF089005	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb AF108696.1 AF108696	Scolomys juruaense cytochrome B (cyt...	50	2e-05
gb AF108685.1 AF108685	Wiedomys pyrrhorhinos cytochrome B (...)	50	2e-05
gb AF108677.1 AF108677	Thomasomys oreas cytochrome B (cytB)...	50	2e-05
gb AF145511.1 AF145511	Melanoplus foedus cytochrome b gene...	50	2e-05
gb AF145511.1 AF145511	Melanoplus angustipennis cytochrome ...	50	2e-05
gb U89627.1 BMU89627	Bolitoglossa macrinosa cytochrome b (cy...	50	2e-05
gb U89623.1 BPU89623	Batrachoseps pacificus cytochrome b (c...	50	2e-05
gb AF181470.1 AF181470	Okapia johnstoni cytochrome b gene...	50	2e-05
gb AF084075.1 AF084075	Lagenorhynchus acutus cytochrome b g...	50	2e-05
gb U90303.1 OMU90303	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90302.1 OMU90302	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90301.1 OMU90301	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90300.1 OMU90300	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb AF038883.1 AF038883	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF039268.1 AF039268	Agkistrodon contortrix cytochrome b ...	50	2e-05
gb AF039267.1 AF039267	Boa constrictor cytochrome b (cytb) ...	50	2e-05
gb S49215.1 S49215	apocytochrome b (sheep, domestic, Merino...	50	2e-05
gb AF158698.1 AF158698	Geomys pinetis cytochrome b gene, co...	50	2e-05
gb AF158692.1 AF158692	Geomys bursarius jugoslavicus cyto...	50	2e-05
gb AF058193.1 AF058193	Ichaginia cruentus cytochrome b (cyt...	50	2e-05
gb AF021629.1 AF021629	Ancilocapra americana cytochrome b (...)	50	2e-05
gb AF022062.1 AF022062	Tragelaphus strepsiceros cytochrome b (cytb)...	50	2e-05
gb AF022062.1 AF022062	Tragelaphus derbianus cytochrome b (cytb) ge...	50	2e-05
gb AF022060.1 AF022060	Hippotragus equinus cytochrome b (cytb) gene...	50	2e-05
gb AF022057.1 AF022057	Tragelaphus oryx cytochrome b (cytb) gene, m...	50	2e-05
gb AF111500.1 AF111500	Lagenorhynchus acutus isolate LACU74...	50	2e-05
gb AF111499.1 AF111499	Lagenorhynchus acutus isolate LACU75...	50	2e-05

gb U69740.1 ESU69740	Lexocemus bicolor cytochrome b (cytb) g...	50	2e-05
gb U69740.1 ESU69740	Eunectes notaeus cytochrome b (cytb) g...	50	2e-05
gb U69740.1 ESU69740	Eunectes murinus cytochrome b (cytb) g...	50	2e-05
gb U69740.1 ESU69740	Epicrates striatus fosteri cytochrome...	50	2e-05
gb U69740.1 ESU69740	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69740.1 ESU69740	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69740.1 ESU69740	Epicrates striatus mceraniei cytochrom...	50	2e-05
gb U69740.1 ESU69740	Epicrates striatus mceraniei cytochrom...	50	2e-05
gb U69740.1 ESU69740	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb U69740.1 ESU69740	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb U69740.1 ESU69740	Epicrates fordii cytochrome b (cytb) ge...	50	2e-05
gb U69740.1 ESU69740	Epicrates fordii cytochrome b (cytb) ge...	50	2e-05
gb U69740.1 ESU69740	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb U69740.1 ESU69740	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb U69740.1 ESU69740	Epicrates angulifer cytochrome b (cytb)...	50	2e-05
gb U69740.1 ESU69740	Epicrates angulifer cytochrome b (cytb)...	50	2e-05
gb U69740.1 ESU69740	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69740.1 ESU69740	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69740.1 ESU69740	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69740.1 ESU69740	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69740.1 ESU69740	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69740.1 ESU69740	Candoia aspera cytochrome b (cytb) gen...	50	2e-05
gb U69740.1 ESU69740	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb U69740.1 ESU69740	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb AF139057.1 AF139057	Isoodon macrourus cytochrome b gene,...	50	2e-05
gb AF090339.1 AF090339	Rhea americana mitochondrion, comple...	50	2e-05
gb AF006275.1 AF006275	Cnemidophorus tigris strain Isla Ang...	50	2e-05
gb AF006275.1 AF006275	Cnemidophorus tigris strain Isla Smi...	50	2e-05
gb AF006275.1 AF006275	Connochaetes taurinus cytochrome b g...	50	2e-05
gb AF028822.1 AF028822	Alcelaphus buselaphus cytochrome b g...	50	2e-05
gb AF028822.1 AF028822	Damaliscus lunatus cytochrome b gene...	50	2e-05
gb AF061340.1 AF061340	Artibeus jamaicensis mitochondrial D...	50	2e-05
gb AF076093.1 AF076093	Thalassarche impavida cytochrome b (...)	50	2e-05
gb AF076093.1 AF076093	Thalassarche carteri cytochrome b (c...	50	2e-05
gb AF076093.1 AF076093	Pelagodroma marina cytochrome b (cyt...	50	2e-05
gb AF076093.1 AF076093	Oceanodroma furcata cytochrome b (cy...	50	2e-05
gb AF076093.1 AF076093	Hydrobates pelagicus cytochrome b (c...	50	2e-05
gb AF076093.1 AF076093	Garrodia nereis cytochrome b (cytb) ...	50	2e-05
gb AF076093.1 AF076093	Fregetta tropica cytochrome b (cytb)...	50	2e-05
gb AF076093.1 AF076093	Diomedea gibsoni cytochrome b (cytb)...	50	2e-05
gb AF076093.1 AF076093	Diomedea epomophora cytochrome b (cy...	50	2e-05
gb AF076093.1 AF076093	Diomedea chionopectera cytochrome b (c...	50	2e-05
gb AF076093.1 AF076093	Diomedea antipodensis cytochrome b (...)	50	2e-05
gb U83314.1 MSU83314	Microhierax semitorquatus cytochrome b (...)	50	2e-05
gb U83314.1 MSU83314	Microhierax erythrogenys cytochrome b ...	50	2e-05
gb U37303.1 SAU37303	Synthliboramphus antiquus cytochrome b...	50	2e-05
gb U37303.1 SAU37303	Ptychoramphus aleuticus cytochrome b g...	50	2e-05
gb U37296.1 CPU37296	Cyclorhynchus psittacula cytochrome b...	50	2e-05
gb U37296.1 CPU37296	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U37296.1 CPU37296	Aethia pygmaea cytochrome b gene, mito...	50	2e-05
gb U37296.1 CPU37296	Aethia pusilla cytochrome b gene, mito...	50	2e-05
gb U37087.1 ACU37087	Aethia cristatella cytochrome b gene, ...	50	2e-05
gb U87525.1 HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87525.1 HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87525.1 HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87525.1 HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U17864.1 STU17864	Saiga tatarica cytochrome b gene, mito...	50	2e-05
gb U17864.1 STU17864	Oreamnos americanus cytochrome b gene...	50	2e-05
gb U17864.1 STU17864	Ovibos moschatus moschatus cytochrome ...	50	2e-05
gb U17864.1 STU17864	Ovis dalli cytochrome b gene, mitochon...	50	2e-05
gb U17864.1 STU17864	Ovis canadensis cytochrome b gene, mit...	50	2e-05
gb U65274.1 TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65274.1 TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65274.1 TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65274.1 TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65274.1 TBU65274	Perognathus amplus cytochrome b (cytb)...	50	2e-05
gb AF034739.1 AF034739	Capra aegagrus cytochrome b (cytb) g...	50	2e-05
gb AF034739.1 AF034739	Capra caucasica cytochrome b (cytb) ge...	50	2e-05
gb AF034739.1 AF034739	Capra cylindricornis cytochrome b (cytb) gen...	50	2e-05
gb AF034739.1 AF034739	Capra falconeri cytochrome b (cytb) ...	50	2e-05
gb AF034739.1 AF034739	Capra ibex cytochrome b (cytb) gene, mitoch...	50	2e-05
gb AF034739.1 AF034739	Ovis aries cytochrome b (cytb) gene...	50	2e-05
gb AF034739.1 AF034739	Ovis vignei cytochrome b (cytb) gene...	50	2e-05

gb AF034724.1	Ovis dalli dalli cytochrome b (cytb) gene. m...	50	2e-05
gb AF034727.1	Ovis ammon darwini cytochrome b (cytb) gene. ....	50	2e-05
gb AF034724.1 AF034724	Pantholops hodgsoni cytochrome b (cy...	50	2e-05
gb AF057132.1 AF057132	Taxidea taxus cytochrome b (cytb) ge...	50	2e-05
gb U94805.1 TMU94805	Trogon melanurus cytochrome b gene, mi...	50	2e-05
gb U94804.1 TCU94804	Trogon comptus cytochrome b gene, mito...	50	2e-05
gb U94803.1 TVU94803	Trogon viridis cytochrome b gene, mito...	50	2e-05
gb AF006231.1 AF006231	Sericossypha albocristata cytochrome...	50	2e-05
gb AF006249.1 AF006249	Pyrrhocoma ruficeps cytochrome b (cy...	50	2e-05
gb AF006238.1 AF006238	Lamprospiza melanoleuca cytochrome b...	50	2e-05
gb AF006234.1 AF006234	Hemispingus atropileus cytochrome b ...	50	2e-05
gb AF005226.1 AF006226	Cypsnagra hirundinacea cytochrome b ...	50	2e-05
gb AF006215.1 AF006215	Chlorophanes spiza cytochrome b (cyt...	50	2e-05
gb AF006214.1 AF006214	Chlorochrysa calliparaea cytochrome ...	50	2e-05
gb AF006213.1 AF006213	Calochaetes coccineus cytochrome b (...)	50	2e-05
gb AF006212.1 AF006212	Buchraupis montana cytochrome b (cyc...	50	2e-05
emb AJ293419.1 RRU293419	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293416.1 RPY293416	Rupicapra pyrenaica pyrenaica mito...	50	2e-05
emb AJ293415.1 RPY293415	Rupicapra pyrenaica parva mitochon...	50	2e-05
emb AJ293414.1 RPY293414	Rupicapra pyrenaica ornata mitochon...	50	2e-05
emb AJ293412.1 RRU293412	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293418.1 CFA293418	Capra falconeri mitochondrial part...	50	2e-05
gb U07578.1 DCU07578	Dasycercus cristicauda mitochondrial c...	50	2e-05
emb AJ004180.1 HPAJ4180	Hydrobates pelagicus mitochondrial ...	50	2e-05
emb Y15695.1 SMY15695	Schilbe mystus mitochondrial cytb gen...	50	2e-05
emb Y15697.1 EDY15697	Eutropius depressirostris mitochondri...	50	2e-05
emb Y15696.1 EDY15696	Eutropius depressirostris mitochondri...	50	2e-05
gb AF015035.1 AF015035	Steatocranus casuarinus 20 cytochrom...	50	2e-05
gb AF015761.1 AF015761	Palmeria dolei cytochrome b (Cytb) g...	50	2e-05
gb AF015758.1 AF015758	Oreomystis mana cytochrome b (Cytb) ...	50	2e-05
gb AF015756.1 AF015756	Vestiaria coccinea cytochrome b (Cyc...	50	2e-05
gb AF015754.1 AF015754	Himatione sanguinea cytochrome b (Cy...	50	2e-05
gb U76052.1 DNU76052	Dromaius novaehollandiae cytochrome b ...	50	2e-05
emb AJ236834.1 CGL236834	Clethrionomys glareolus mitochondr...	50	2e-05
gb U83158.1 POU83158	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb U83157.1 POU83157	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb U83156.1 AAU83156	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83155.1 AAU83155	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83154.1 AAU83154	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83156.1 CLU83156	Chelodina longicollis cytochrome b gen...	50	2e-05
emb AJ277676.1 ESC277676	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277675.1 ESC277675	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277672.1 ELO277672	Elaphe longissima mitochondrial pa...	50	2e-05
emb AJ277671.1 ELO277671	Elaphe longissima mitochondrial pa...	50	2e-05
emb Y11832.1 MTNCOMGN	Dasypus novemcinctus complete mitoch...	50	2e-05
emb AJ388467.1 NBA388467	Nemacheilus barbatulus mitochondria...	50	2e-05
emb AJ388468.1 IME388468	Ictalurus melas mitochondrial cyt b...	50	2e-05
emb AJ388459.1 LDE388459	Leucaspius delineatus mitochondrial...	50	2e-05
gb U46167.1 SCU46167	Sciurus carolinensis cytochrome b gene...	50	2e-05
emb AJ245673.1 SIN245673	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245638.1 SIN245638	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245678.1 EDE245678	Eutropius depressirostris partial ...	50	2e-05
emb AJ245677.1 EDE245677	Eutropius depressirostris partial ...	50	2e-05
emb AJ245676.1 EDE245676	Eutropius depressirostris partial ...	50	2e-05
emb AJ245675.1 EDE245675	Eutropius depressirostris partial ...	50	2e-05
emb AJ245674.1 EDE245674	Eutropius depressirostris partial ...	50	2e-05
emb Y15884.3 MTRACOMPL	Rhea americana complete mitochondria...	50	2e-05
gb U60768.1 PCU60768	Parus cinctus cytochrome b gene, mito...	50	2e-05
gb U48955.1 TMU48955	Thalassarche melanophris melanophris c...	50	2e-05
gb U48954.1 TCU48954	Thalassarche chrysostoma cytochrome b ...	50	2e-05
gb U48944.1 TCU48944	Thalassarche chlororhynchus chlororhyn...	50	2e-05
gb U48943.1 PPU48943	Phoebastria palpebrata cytochrome b (cy...	50	2e-05
gb U48942.1 PFU48942	Phoebastria fusca cytochrome b (cytb) g...	50	2e-05
gb U48941.1 MCU48941	Macronectes giganteus cytochrome b (cy...	50	2e-05
gb U48947.1 DEU48947	Diomedea exulans dabbenena cytochrome ...	50	2e-05
gb U48946.1 DEU48946	Diomedea epomophora sanfordi cytochrom...	50	2e-05
gb U48949.1 DAU48949	Diomedea amsterdamensis cytochrome b (...)	50	2e-05
gb U55509.1 APU55509	Artibeus planirostris cytochrome b (cy...	50	2e-05
gb U55507.1 AQU55507	Artibeus obscurus cytochrome b (cytb) ...	50	2e-05
gb U55506.1 AQU55506	Artibeus obscurus cytochrome b (cytb) ...	50	2e-05



gb U66505.1 ALUG6505	Artibeus lituratus cytochrome b (cytb)...	50	2e-05
gb U66504.1 AJU66504	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb U66503.1 AJU66503	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb U66502.1 AIU66502	Artibeus intermedius cytochrome b (cyt...	50	2e-05
gb U66501.1 AU66501	Artibeus inopinatus cytochrome b (cytb...	50	2e-05
gb U66500.1 AHU66500	Artibeus hirsutus cytochrome b (cytb)...	50	2e-05
gb U66499.1 AFU66499	Artibeus fraterculus cytochrome b (cyt...	50	2e-05
gb U66498.1 AFU66499	Artibeus fimbriatus cytochrome b (cytb...	50	2e-05
gb U63061.1 BBU63061	Brachyramphus brevirostris cytochrome...	50	2e-05
gb U63060.1 BBU63060	Brachyramphus brevirostris cytochrome...	50	2e-05
gb U63059.1 BBU63059	Brachyramphus brevirostris cytochrome...	50	2e-05
gb U63058.1 BBU63058	Brachyramphus brevirostris cytochrome...	50	2e-05
gb U58386.1 SJU58386	Scolomys juruaense cytochrome b (cyt-b...	50	2e-05
gb L11905.1 CGYMTCTBD	Cratogeomys gymnotus mitochondrial c...	50	2e-05
gb U34672.1 MNU34672	Metachirus nudicaudatus cytochrome b l...	50	2e-05
gb U34671.1 MNU34671	Metachirus nudicaudatus cytochrome b l...	50	2e-05
emb Y14951.1 MTY14951	Capreolus capreolus mitochondrial cyt...	50	2e-05
emb Y14371.1 MTCCCYTB	Capreolus capreolus mitochondrial cyt...	50	2e-05
gb L11909.1 CGYMTCTBH	Cratogeomys tylosinus mitochondrial...	50	2e-05
gb L11901.1 PPGMYCTBB	Geomys bursarius jugosicircularis mito...	50	2e-05
gb L11904.1 CGYMTCTBC	Cratogeomys goldmani goldmani mitoch...	50	2e-05
emb X94928.1 SPCYTB	S. putorius mitochondrial DNA for cytoch...	50	2e-05
gb U46770.1 ARU46770	Anthus richardi cytochrome b gene, mit...	50	2e-05
gb U46769.1 ABU46769	Anthus berthelotii cytochrome b gene, ...	50	2e-05
gb U46183.1 SSU46183	Sciurus stramineus cytochrome b gene, ...	50	2e-05
emb Y10728.1 PSMY10728	P. schwarzi mitochondrial cytb gene, ...	50	2e-05
emb X95768.1 NLMCB	N. leucopterus mitochondrial cytochrome b...	50	2e-05
emb X95767.1 NGRIMCB	N. griseus mitochondrial cytochrome b gene	50	2e-05
emb X86763.1 MTVGCYT26	V. gryphus mitochondrial cytb gene	50	2e-05
emb X86754.1 MTLCCYT17	L. crumeniferus mitochondrial cytb gene	50	2e-05
emb X86743.1 MTCACYT6	C. aura mitochondrial cytb gene	50	2e-05
dbj AB035242.1 AB035242	Pantodon buchholzi mitochondrial cy...	50	2e-05
emb X60946.1 MITDCB33	T. dorbignyi mitochondrial gene for c...	50	2e-05
emb AJ000029.1 MIRTCYB29	Rangifer tarandus mitochondrial cy...	50	2e-05
emb X82302.1 MIPFCYTBG	P. fasciata mitochondrial cytochrome...	50	2e-05
emb X56291.1 MIOHCYTB	O. hemionus mitochondrial cytb gene fo...	50	2e-05
emb X56284.1 MIOACYTB	O. aries mitochondrial cytb gene for c...	50	2e-05
emb AJ000022.1 MIMSCYB22	Dama dama mitochondrial cytb gene	50	2e-05
emb X72005.1 MILWCYTB	L. weddelli mitochondrial gene for cyt...	50	2e-05
emb Y08814.1 MIHLCYTBG	H. liberiensis mitochondrial cytochro...	50	2e-05
emb X60942.1 MIGTCB31	Gymnorhina tibicen mitochondrial gene...	50	2e-05
emb X56290.1 MIDDCYTB	D. dama mitochondrial cytb gene for cy...	50	2e-05
emb AJ000021.1 MICECYB21	Cervus elaphus mitochondrial cytb...	50	2e-05
emb AJ000024.1 MICCCYB24	Capreolus capreolus mitochondrial...	50	2e-05
emb V00654.1 MI3TXX	Bos taurus complete mitochondrial genome	50	2e-05
emb X56286.1 MIAACYTB	A. americana mitochondrial cytb gene...	50	2e-05
gb L19718.1 AJUMTCYTB	Artibeus lituratus mitochondrial cyto...	50	2e-05
gb U27543.1 BRU27543	Balearica regulorum cytochrome b (cytb...	50	2e-05
dbj AB030025.1 AB030025	Sciurus stramineus mitochondrial cy...	50	2e-05
gb U18258.1 SCU18258	Spharagemon campestris cytochrome b ge...	50	2e-05
gb U18257.1 SCU18257	Spharagemon collare cytochrome b gene...	50	2e-05
gb U18253.1 TPU18253	Trimerotropis picturaria cytochrome b...	50	2e-05
gb U18250.1 CPU18250	Camnula pellucida cytochrome b gene, m...	50	2e-05
gb U17904.1 CCU17904	Circotettix carlinianus mitochondrial...	50	2e-05
dbj D84202.1 GOTMTCB8	Capra falconeri mitochondrial DNA for...	50	2e-05
dbj D82889.1 D82889	Bos javanicus mitochondrial DNA for cyt...	50	2e-05
dbj D32195.1 CCRMTCB25	Capricornis sumatrensis mitochondrial...	50	2e-05
dbj D32191.1 CCRMTCB21	Capricornis crispus mitochondrial ge...	50	2e-05
dbj AB021098.1 AB021098	Cervus elaphus kansuensis mitochondr...	50	2e-05
dbj AB021097.1 AB021097	Cervus elaphus xanthopygus mitochon...	50	2e-05
dbj AB021095.1 AB021095	Cervus nippon yezoensis mitochondri...	50	2e-05
dbj AB021094.1 AB021094	Cervus nippon centralis mitochondri...	50	2e-05
dbj AB021092.1 AB021092	Cervus nippon mageshimae mitochondr...	50	2e-05
dbj AB021091.1 AB021091	Cervus nippon keramae mitochondrial...	50	2e-05
dbj AB001612.1 AB001612	Cervus elaphus mitochondrial DNA fo...	50	2e-05
dbj D84205.1 SHPMTCB6	Sheep mitochondrial DNA for cytochrom...	50	2e-05
dbj D84203.1 SHPMTCB3	Ovis musimon mitochondrial DNA for cy...	50	2e-05
dbj D74456.1 BOVMTCB8	Bos javanicus mitochondrial gene for...	50	2e-05
dbj D74455.1 BOVMTCB	Bovine mitochondrial gene for cytochr...	50	2e-05
dbj D72178.1 ORMTCB28	Oreamnos americanus mitochondrial ge...	50	2e-05
dbj D72175.1 NAGMTCB26	Nemotardus goral mitochondrial gene...	50	2e-05

dbj D32182.1 CEUMTC011	Cervus nippon mitochondrial gene for...	50	2e-05
dbj AB021094.1 AB021094	Cervus elaphus scoticus mitochondri...	50	2e-05
dbj AB021090.1 AB021090	Cervus elaphus canadensis mitochond...	50	2e-05
dbj AB021093.1 AB021093	Cervus nippon nippon mitochondrial ...	50	2e-05
dbj AB021090.1 AB021090	Cervus nippon pulchellus mitochondr...	50	2e-05
dbj AB006539.1 AB006539	Dinodon semicarinatus mitochondrial...	50	2e-05
dbj AB006800.1 AB006800	Ovis aries mitochondrial DNA for cy...	50	2e-05
gb L12763.1 LDHMTCTB	Lepidochelys kempi (LK-3) mitochondri...	50	2e-05
gb L08032.1 CPLMTCYT5A	Carcharhinus plumbeus mitochondrial ...	50	2e-05
gb L28941.1 URRCYS	Uroderma bilobatum cytochrome b gene, 5'...	50	2e-05
gb L28937.1 CDECYB	Chiorderma doriae cytochrome b gene, 5' end	50	2e-05
emb AJ010056.1 CPY010056	Capra pyrenaica (individual 12) mi...	50	2e-05
emb AJ010054.1 CPY010054	Capra pyrenaica (individual 11) mi...	50	2e-05
emb AJ010053.1 CPY010053	Capra pyrenaica (individual 10) mi...	50	2e-05
emb AJ010052.1 CPY010052	Capra pyrenaica (individual 9) mit...	50	2e-05
emb AJ010051.1 CPY010051	Capra pyrenaica (individual 8) mit...	50	2e-05
emb AJ010050.1 CPY010050	Capra pyrenaica (individual 7) mit...	50	2e-05
emb AJ010049.1 CPY010049	Capra pyrenaica (individual 6) mit...	50	2e-05
emb AJ010048.1 CPY010048	Capra pyrenaica (individual 5) mit...	50	2e-05
emb AJ010047.1 CPY010047	Capra pyrenaica (individual 4) mit...	50	2e-05
emb X95777.1 CLMCB	C. longirostris mitochondrial cytochrome ...	50	2e-05
emb AJ009879.1 CIB9879	Capra ibex nubiana mitochondrial cyt...	50	2e-05
emb AJ010055.1 CIB010055	Capra ibex (individual 1) ibex mit...	50	2e-05
gb U08946.1 CAU08946	Coragyps atratus mitochondrion cytochr...	50	2e-05
gb U08945.1 CBU08945	Cathartes burrovianus mitochondrion cy...	50	2e-05
gb U08944.1 VGU08944	Vultur gryphus mitochondrion cytochrom...	50	2e-05
gb U08941.1 PAU08941	Platalea alba mitochondrion cytochrome...	50	2e-05
gb U08940.1 PRU08940	Phoenicopterus ruber mitochondrion cyt...	50	2e-05
emb X95775.1 ACMCB	A. cristatus mitochondrial cytochrome b gene	50	2e-05
emb X95774.1 ABMCB	A. bennettii mitochondrial cytochrome b gene	50	2e-05
emb X95764.1 AAMCB	A. albertisi mitochondrial cytochrome b gene	43	8e-05
gb AF040383.1 AF040383	Alces alces cytochrome b (cytb) gene...	46	3e-04
gb AF232023.1 AF232023	Tamandua tetradactyla clone 7 cytoch...	46	3e-04
gb AF232022.1 AF232022	Tamandua tetradactyla clone 6 mitoch...	46	3e-04
gb AF232021.1 AF232021	Tamandua tetradactyla clone 5 cytoch...	46	3e-04
gb AF157466.1 AF157466	Lepus timidus cytochrome b (Cyb) gen...	46	3e-04
gb AF157465.1 AF157465	Lepus granatensis cytochrome b (Cyb)...	46	3e-04
gb AF157464.1 AF157464	Lepus corsicanus haplotype 1 cytochr...	46	3e-04
gb AF157463.1 AF157463	Lepus corsicanus haplotype 3 cytochr...	46	3e-04
gb AF157460.1 AF157460	Lepus europaeus cytochrome b (Cyb) g...	46	3e-04
gb AF231664.1 AF231664	Tylosurus crocodilus crocodilus cyto...	46	3e-04
gb AF231663.1 AF231663	Tylosurus crocodilus clone STR1-1937...	46	3e-04
gb AF231662.1 AF231662	Tylosurus crocodilus clone H3-156 cy...	46	3e-04
gb AF231660.1 AF231660	Tylosurus acus pacificus cytochrome ...	46	3e-04
gb AF231659.1 AF231659	Tylosurus acus melanotus clone STR1...	46	3e-04
gb AF231658.1 AF231658	Tylosurus acus melanotus clone STR1...	46	3e-04
gb AF231657.1 AF231657	Tylosurus acus imperialis cytochrome...	46	3e-04
gb AF231656.1 AF231656	Tylosurus acus acus cytochrome b oxi...	46	3e-04
gb AF231644.1 AF231644	Strongylura hubbsi cytochrome b oxid...	46	3e-04
gb AF231639.1 AF231639	Ablennes hians cytochrome b oxidase ...	46	3e-04
gb AF232019.1 AF232019	Tamandua tetradactyla clone 3 cytoch...	46	3e-04
gb AF232017.1 AF232017	Tamandua tetradactyla clone 1 cytoch...	46	3e-04
gb AF232014.1 AF232014	Myiodon darwini cytochrome b gene...	46	3e-04
gb AF118564.1 AF118564	Alligator mississippiensis isolate S...	46	3e-04
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gb AF118562.1 AF118562	Alligator mississippiensis isolate S...	46	3e-04
gb AF118561.1 AF118561	Alligator mississippiensis isolate G...	46	3e-04
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gb AF118559.1 AF118559	Alligator mississippiensis isolate A...	46	3e-04
gb AF118558.1 AF118558	Alligator mississippiensis isolate A...	46	3e-04
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gb AF118550.1 AF118550	Alligator mississippiensis isolate F...	46	3e-04
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gb AF118548.1 AF118548	Alligator mississippiensis isolate F...	46	3e-04
gb AF118547.1 AF118547	Sorex monticolus specimen-voucher AF...	46	3e-04

gb AF126272.1 AF126272	Myospalax myospalax cytochrome b (cy...	46	3e-04
gb AF126271.1 AF126271	Myospalax psilurus isolate 2 cytochr...	46	3e-04
gb AF126270.1 AF126270	Myospalax psilurus isolate 1 cytochr...	46	3e-04
gb AF126266.1 AF126266	Eospalax fontanierii isolate 4 cytoc...	46	3e-04
emb AJ004340.1 ADAJ4340	Acrocephalus dumetorum mitochondria...	44	0.001
emb AJ004264.1 ADAJ4264	Acrocephalus dumetorum mitochondria...	44	0.001

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<u>D12195</u>	243	.....	267
<u>D12191</u>	398	.....	422
<u>AB021028</u>	398	.....	422
<u>AB021027</u>	398	.....	422
<u>AB021025</u>	398	.....	422
<u>AB021024</u>	398	.....	422
<u>AB021022</u>	398	.....	422
<u>AB021021</u>	398	.....	422



<u>AB001612</u>	398	.....	422
<u>D84205</u>	398	.....	422
<u>D84203</u>	398	.....	422
<u>D34636</u>	398	.....	422
<u>D34635</u>	398	.....	422
<u>D32198</u>	243	.....	267
<u>D32196</u>	243	.....	267
<u>D32192</u>	398	.....	422
<u>AB021099</u>	398	.....	422
<u>AB021096</u>	398	.....	422
<u>AB021093</u>	398	.....	422
<u>AB021090</u>	398	.....	422
<u>AB008539</u>	15302	.....	15326
<u>AB006800</u>	398	.....	422
<u>L12763</u>	260	.....	284
<u>L08032</u>	401	.....	425
<u>L28941</u>	398	.....	422
<u>L28937</u>	398	.....	422
<u>AJ010056</u>	269	.....	293
<u>AJ010054</u>	269	.....	293
<u>AJ010053</u>	269	.....	293
<u>AJ010052</u>	269	.....	293
<u>AJ010051</u>	269	.....	293
<u>AJ010050</u>	269	.....	293
<u>AJ010049</u>	269	.....	293
<u>AJ010048</u>	269	.....	293
<u>AJ010047</u>	269	.....	293
<u>X95777</u>	407	.....	431
<u>AJ009879</u>	269	.....	293
<u>AJ010055</u>	269	.....	293
<u>U08946</u>	303	.....	327
<u>U08945</u>	303	.....	327
<u>U08944</u>	303	.....	327
<u>U08941</u>	303	.....	327
<u>U08940</u>	303	.....	327
<u>X95775</u>	303	.....	327
<u>X95774</u>	303	.....	327
<u>X95764</u>	303	.....	327
<u>AF040383</u>	287	.....	310
<u>AF232023</u>	400	.....	422
<u>AF232022</u>	400	.....	422
<u>AF232021</u>	400	.....	422
<u>AF157466</u>	322	.....	344
<u>AF157465</u>	324	.....	346
<u>AF157464</u>	324	.....	346
<u>AF157463</u>	324	.....	346
<u>AF157460</u>	321	.....	343
<u>AF231664</u>	400	.....	422
<u>AF231663</u>	400	.....	422
<u>AF231662</u>	400	.....	422
<u>AF231660</u>	400	.....	422
<u>AF231659</u>	400	.....	422
<u>AF231658</u>	400	.....	422
<u>AF231657</u>	400	.....	422
<u>AF231656</u>	400	.....	422
<u>AF231644</u>	400	.....	422
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<u>AF232019</u>	400	.....	422
<u>AF232017</u>	400	.....	422
<u>AF232014</u>	400	.....	422
<u>AF118564</u>	345	.....	367
<u>AF118563</u>	345	.....	367
<u>AF118562</u>	344	.....	366
<u>AF118561</u>	344	.....	366
<u>AF118560</u>	344	.....	366
<u>AF118559</u>	344	.....	366
<u>AF118558</u>	344	.....	366
<u>AF118557</u>	381	.....	403
<u>AF118556</u>	381	.....	403
<u>AF118555</u>	381	.....	403
<u>AF118554</u>	381	.....	403

<u>AF118551</u>	381	.....	403
<u>AF118552</u>	381	.....	403
<u>AF118551</u>	381	.....	403
<u>AF118550</u>	381	.....	403
<u>AF118549</u>	381	.....	403
<u>AF118548</u>	381	.....	403
<u>AF238041</u>	400	.....	422
<u>AF326272</u>	400	.....	422
<u>AF326271</u>	400	.....	422
<u>AF326270</u>	400	.....	422
<u>AF326266</u>	400	.....	422
<u>AJ004340</u>	302	....n.....	326
<u>AJ004264</u>	302	....n.....	326

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 39355

Number of Sequences: 807597

Number of extensions: 39355

Number of successful extensions: 15066

Number of sequences better than 10.0: 5706

length of query: 25

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 8

effective length of database: 2,850,098,736

effective search space: 22800789888

effective search space used: 22800789888

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

**Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.**



**BLASTN 2.1.2 [Nov-13-2000]**

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query-

(26 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports

**Distribution of 500 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

	Score	E Value
qb AF189111.1 AF189111	52	6e-06
qb U86834.1 U86834	52	6e-06
qb AF123633.1 AF123633	52	6e-06
qb AF123617.1 AF123617	52	6e-06
qb AF127202.1 AF127202	52	6e-06
qb AF127194.1 AF127194	52	6e-06
qb AF217828.1 AF217828	52	6e-06
qb AF160578.1 AF160578	52	6e-06
qb AF009931.2 AF009931	52	6e-06
qb AF091629.1 AF091629	52	6e-06
qb AF034967.1	52	6e-06
qb AF038290.1 AF038290	52	6e-06
qb U07577.1 AMU07577	52	6e-06
qb U81343.1 CFU81343	52	6e-06
emb AJ222681.1 ABCYTOB	52	6e-06
qb M99464.1 PNZMTCYTB	52	6e-06
emb AJ225116.1 DNJ225116	52	6e-06
qb U25738.1 PRU25738	52	6e-06
qb U25736.1 PRU25736	52	6e-06
qb U15202.1 SMU15202	52	6e-06
qb U15204.1 PRI15204	52	6e-06
emb X56290.1 MIDDCYTB	52	6e-06
emb X56286.1 MTAACYTBA	52	6e-06
dbj D88639.1 D88639	52	6e-06
dbj D82890.1 D82890	52	6e-06
qb AF119261.1 AF119261	46	3e-04
qb AF123615.1 AF123615	46	3e-04
qb AF160603.1 AF160603	46	3e-04
qb U62697.1 CCOLCYTB2	46	3e-04
qb U62685.1 CSICCYTB2	46	3e-04
qb AF022071.1	46	3e-04
qb AF022070.1	46	3e-04
qb U83317.1 PSU83317	46	3e-04
qb U37293.1 CCU37293	46	3e-04
qb U37292.1 CCU37292	46	3e-04
qb U37291.1 BMU37291	46	3e-04
qb AF082055.1 AF082055	46	3e-04
qb U72770.1 JMU72770	46	3e-04
qb U07578.1 DCU07578	46	3e-04
qb AF011908.1 GOCCCYTB1	46	3e-04
emb AJ004231.1 SBAJ4231	46	3e-04
emb AJ004230.1 SBAJ4230	46	3e-04
emb AJ004229.1 SBAJ4229	46	3e-04
emb AJ004232.1 SBAJ4232	46	3e-04
qb U88865.1	46	3e-04
qb U90001.1 MBU90001	46	3e-04
qb U63057.1 BMU63057	46	3e-04
dbj AB036404.1 AB036404	46	3e-04
dbj AB036402.1 AB036402	46	3e-04
dbj AB036400.1 AB036400	46	3e-04
dbj AB036398.1 AB036398	46	3e-04
qb U19611.1 JMU19611	46	3e-04
emb X92519.1 HACYTB	46	3e-04
qb U08014.1 GAEMTCYTB	46	3e-04
qb U08011.1 CPLMTCYTB	46	3e-04
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qb AY005212.1	44	0.001
qb AY005211.1	44	0.001
qb AF187122.1 AF187122	44	0.001
qb AF187120.1 AF187120	44	0.001
qb AF187119.1 AF187119	44	0.001
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qb AF221272.1 AF221272	44	0.001

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gb AF081977.1 AF081977	Vireo cassinii cassinii specimen-vou...	44	0.001
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gb AF081975.1 AF081975	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081974.1 AF081974	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081973.1 AF081973	Vireo cassinii cassinii specimen-vou...	44	0.001
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gb AF081960.1 AF081960	Vireo leucophrys leucophrys specimen...	44	0.001
gb AF081959.1 AF081959	Vireolanius leucotis leucotis cytoch...	44	0.001
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gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	44	0.001
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gb AF283619.1 AF283619	Elaphe obsoleta LSUMZJ39162 cytochrom...	44	0.001
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gb AF283602.1 AF283602	Elaphe obsoleta LSUMZ H3388 cytochro...	44	0.001
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gb AF146616.1 AF146616	Actophilornis africanus cytochrome b...	44	0.001
gb AF271410.1 AF271410	Galago moholi cytochrome b (cyt b) g...	44	0.001
gb AF290139.1 AF290139	Peucedramus taeniatus cytochrome b (...)	44	0.001
ref NC 002504.1	Lama pacos mitochondrion, complete genome	44	0.001
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gb AF123634.1 AF123634	Pyroderus scutatus cytochrome b gene...	44	0.001
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gb AF042718.1	Muntiacus muntjak cytochrome b gene, mitoch...	44	0.001
gb AF042717.1 AF042717	Stenella coeruleoalba cytochrome b g...	44	0.001
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gb AF157915.1 AF157915	Spermophilus richardsoni isolate S63...	44	0.001
gb AF157914.1 AF157914	Spermophilus richardsoni isolate S62...	44	0.001
gb AF157912.1 AF157912	Spermophilus undulatus isolate S60 c...	44	0.001
gb AF157906.1 AF157906	Spermophilus undulatus isolate S55 c...	44	0.001
gb AF157891.1 AF157891	Spermophilus elegans elegans isolate...	44	0.001
gb AF157882.1 AF157882	Spermophilus columbianus columbianus...	44	0.001
gb AF157859.1 AF157859	Spermophilus citellus isolate S118 c...	44	0.001
gb AF157858.1 AF157858	Spermophilus citellus isolate S117 c...	44	0.001
gb AF157839.1 AF157839	Spermophilus elegans elegans isolate...	44	0.001
gb AF030497.1 AF030497	Crocidura brunnea cytochrome b (cyt ...	44	0.001
gb U03541.2 LAU03541	Lenoxus apicalis cytochrome b gene, pa...	44	0.001
gb AF009951.2 AF009951	Heros appendiculatus cytochrome b (c...	44	0.001
gb AF009941.1 AF009941	Tomocichla tuba cytochrome b (cytb) ...	44	0.001
gb AF009925.1 AF009925	Archocentrus sajica cytochrome b (cy...	44	0.001
gb AF094633.1 AF094633	Stachyris whiteheadi cytochrome b ge...	44	0.001
gb AF094621.1 AF094621	Eminia lepida cytochrome b gene, par...	44	0.001
gb AF094618.1 AF094618	Hypergerus atriceps cytochrome b gen...	44	0.001
gb AF166348.1 AF166348	Phascolarctos cinereus cytochrome b ...	44	0.001
gb AF158697.1 AF158697	Geomys bursarius ozarkensis cytochro...	44	0.001
gb AF158694.1 AF158694	Geomys bursarius majusculus cytochro...	44	0.001
gb AF158693.1 AF158693	Geomys bursarius bursarius cytochrom...	44	0.001
gb AF158688.1 AF158688	Geomys bursarius missouriensis cytoc...	44	0.001
gb AF100720.1 AF100720	Spermophilus citellus cytochrome b (...	44	0.001
gb AF091632.1 AF091632	Bubalus depressicornis cytochrome b ...	44	0.001
gb AF102815.1 AF102815	Dromiciops gliroides cytochrome b ge...	44	0.001
gb AF102814.1 AF102814	Vombatus ursinus cytochrome b gene, ...	44	0.001
gb AF022065.1	Tragelaphus euryceros cytochrome b (cytb) ge...	44	0.001
gb AF022059.1	Kobus ellipsiprymnus cytochrome b (cytb) gen...	44	0.001
gb AF022058.1	Antilope cervicapra cytochrome b (cytb) gene...	44	0.001
gb AF022057.1	Tragelaphus oryx cytochrome b (cytb) gene, m...	44	0.001
gb AF022054.1	Antidorcas marsupialis cytochrome b (cytb) g...	44	0.001
gb AF016637.1 AF016637	Connochaetes gnou cytochrome b (cytb...	44	0.001
gb U69863.1 PSU69863	Python sebae cytochrome b (cytb) gene,...	44	0.001
gb U69844.1 LTU69844	Lichanura trivirgata cytochrome b (cyt...	44	0.001
gb AF143193.1 AF143193	Epinephelus sp. cytochrome b (cytb) ...	44	0.001
gb AF121222.1 AF121222	Amphiprion ocellaris isolate 8 cytoc...	44	0.001
gb AF096625.1 AF096625	Kobus ellipsiprymnus defassa cytochr...	44	0.001
gb AF096624.1 AF096624	Kobus ellipsiprymnus ellipsiprymnus c...	44	0.001
gb AF081052.1 AF081052	Eulemur rubriventer cytochrome b (cy...	44	0.001
gb AF081049.1 AF081049	Eulemur macaco macaco cytochrome b (...	44	0.001
gb AF081048.1 AF081048	Eulemur fulvus albifrons cytochrome ...	44	0.001
gb AF082063.1 AF082063	Elminia longicauda cytochrome b gene...	44	0.001
emb AJ010957.1 HAAJ10957	Hippopotamus amphibius complete mi...	44	0.001
gb U76506.1 CLU76506	Chlamydera lauterbachii cytochrome b g...	44	0.001
gb U76504.1 CCU76504	Chlamydera cerviniventris cytochrome b...	44	0.001
gb U76505.1 ASU76505	Amblyornis subalaris cytochrome b gene...	44	0.001
gb U76503.1 APU76503	Archboldia papuensis cytochrome b gene...	44	0.001
gb U76508.1 AIU76508	Amblyornis inornatus cytochrome b gene...	44	0.001
gb AF014969.1 AF014969	Connochaetes taurinus cytochrome b g...	44	0.001
gb AF051876.1 AF051876	Rhodeus ocellatus cytochrome b (cytb...	44	0.001
gb AF082007.1 AF082007	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082006.1 AF082006	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082005.1 AF082005	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082004.1 AF082004	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082003.1 AF082003	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082002.1 AF082002	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082001.1 AF082001	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082000.1 AF082000	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081999.1 AF081999	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081998.1 AF081998	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081997.1 AF081997	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081996.1 AF081996	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081995.1 AF081995	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081994.1 AF081994	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081993.1 AF081993	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081992.1 AF081992	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081991.1 AF081991	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081990.1 AF081990	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081989.1 AF081989	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081988.1 AF081988	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081987.1 AF081987	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081986.1 AF081986	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081985.1 AF081985	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081984.1 AF081984	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081983.1 AF081983	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081982.1 AF081982	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081981.1 AF081981	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081980.1 AF081980	Vireo plumbeus plumbeus specimen-vou...	44	0.001



gb AF081991.1 AF081991	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb S71150.1 S71150	cytochrome b (Spermophilus richardsonii=...	44	0.001
gb AF012235.1 AF012235	Cryptomys hottentotus natalensis cyt...	44	0.001
gb U53580.1 NCU53580	Nycticebus coucang cytochrome b (cyt b...	44	0.001
gb U53577.1 EFU53577	Eulemur fulvus rufus cytochrome b (cyt...	44	0.001
gb U53576.1 EFU53576	Eulemur fulvus collaris cytochrome b (...)	44	0.001
gb U95512.1 ESERCYTB2	Eptesicus serotinus 3' cytochrome b (...)	44	0.001
gb U95508.1 PKUHLCTB2	Pipistrellus kuhli 5' cytochrome b (...)	44	0.001
gb U17868.1 BTU17868	Budorcas taxicolor taxicolor cytochrom...	44	0.001
gb U17867.1 BTU17867	Budorcas taxicolor bedfordi cytochrome...	44	0.001
gb U17860.1 ODU17860	Ovis dalli cytochrome b gene, mitochon...	44	0.001
gb U17859.1 OCU17859	Ovis canadensis cytochrome b gene, mit...	44	0.001
emb AJ010556.1 ASP010556	Acomys spinosissimus mitochondrial...	44	0.001
gb AF034736.1 AF034736	Capra falconeri cytochrome b (cytb) ...	44	0.001
gb AF034730.1 AF034730	Ovis aries cytochrome b (cytb) gene, ...	44	0.001
gb AF034729.1 AF034729	Ovis vignei cytochrome b (cytb) gene...	44	0.001
gb AF034728.1	Ovis dalli dalli cytochrome b (cytb) gene, m...	44	0.001
gb AF034727.1	Ovis ammon darwini cytochrome b (cytb) gene, ...	44	0.001
gb AF034724.1 AF034724	Pantholops hodgsoni cytochrome b (cy...	44	0.001
gb AF034722.1 AF034722	Addax nasomaculatus cytochrome b (cy...	44	0.001
gb U72038.1 MMU72038	Monodon monoceros cytochrome b (cytb), ...	44	0.001
gb U72037.1 DLU72037	Delphinapterus leucas cytochrome b (cy...	44	0.001
gb M99455.1 MUXMTCYTB	Murexia longicaudata cytochrome b gen...	44	0.001
gb L29055.1 SHEMTDLOOP	Sheep mitochondrial cytochrome b (Cy...	44	0.001
gb AF082047.1 AF082047	Coccyzus americanus cytochrome b gen...	44	0.001
gb AF038286.1 AF038286	Antechinus minimus cytochrome b gene...	44	0.001
gb AF038284.1 AF038284	Antechinus swainsonii cytochrome b g...	44	0.001
gb AF059093.1 AF059093	Anas undulata cytochrome b gene, par...	44	0.001
gb AF059092.1 AF059092	Anas superciliosa rogersi cytochrome...	44	0.001
gb AF059091.1 AF059091	Anas sparsa cytochrome b gene, parti...	44	0.001
gb AF059080.1 AF059080	Anas melleri cytochrome b gene, part...	44	0.001
gb AF059078.1 AF059078	Anas laysanensis cytochrome b gene, ...	44	0.001
gb AF052240.1 AF052240	Anairetes flavirostris cytochrome b ...	44	0.001
gb AF006240.1 AF006240	Mitrospingus cassinii cytochrome b (...)	44	0.001
gb AF006227.1 AF006227	Dacnis cayana cytochrome b (cytb) ge...	44	0.001
gb AF047447.1 AF047447	Oryx leucoryx cytochrome b gene, mit...	44	0.001
gb U07576.1 AHU07576	Antechinus habbema mitochondrial cytoc...	44	0.001
gb AF028180.1 AF028180	Urocyon cinereoargenteus cytochrome ...	44	0.001
gb AF028178.1 AF028178	Pseudalopex sechurae cytochrome b (c...	44	0.001
gb AF028170.1 AF028170	Vulpes zerda cytochrome b (cytb) gen...	44	0.001
gb M99454.1 ASWMTSCYTB	Antechinus stuartii cytochrome b gen...	44	0.001
gb M99453.1 ASWMTCYTB	Antechinus swainsonii cytochrome b ge...	44	0.001
gb U23461.1 ANU23461	Antechinus naso cytochrome b gene, mit...	44	0.001
gb U87138.1 TVU87138	Trichosurus vulpecula cytochrome b (cy...	44	0.001
gb U07590.1 PMU07590	Planigale maculata mitochondrial cytoc...	44	0.001
emb AJ004326.1 PTAJ4326	Phylloscopus trochilus mitochondria...	44	0.001
gb AF020255.1 AF020255	Cyclura nubila cytochrome b (cytb) g...	44	0.001
emb Y19184.1 LPA19184	Lama pacos complete mitochondrial genome	44	0.001
gb U88862.1	Amphilophus citrinellum cytochrome b (cytb) ge...	44	0.001
gb U88859.1	Thorichthys aureum cytochrome b (cytb) gene, m...	44	0.001
gb U88858.1	Thorichthys cf. aureum cytochrome b (cytb) gen...	44	0.001
gb U88857.1	Kerichthys labridens cytochrome b (cytb) gene, ...	44	0.001
gb U88856.1	Kerichthys carpintis cytochrome b (cytb) gene, ...	44	0.001
emb Y10524.1 MIMRGEN	Macropus robustus complete mitochondri...	44	0.001
gb U81357.1 CSU81357	Chelydra serpentina cytochrome b gene...	44	0.001
gb U81356.1 CLU81356	Chelodina longicollis cytochrome b gen...	44	0.001
gb U75354.1 LUU75354	Leptomyrmex unicolor cytochrome b gene...	44	0.001
gb U77332.1 GCU77332	Gymnorhinus cyanocephala cytochrome-b ...	44	0.001
emb Z29571.1 QVMTGNME	Didelphis virginiana complete mitoch...	44	0.001
emb AJ222679.1 BTCYTO8	Soselaphus tragocamelus mitochondria...	44	0.001
emb AJ222680.1 TSCYTO8	Tragelaphus spekii mitochondrial cyt...	44	0.001
emb AJ222685.1 ODCYTO8	Oryx dammah mitochondrial cytochrome...	44	0.001
gb M22466.1 PMLMTCYTB	Perameles nasuta cytochrome b gene, c...	44	0.001
gb M22453.1 THVMTCYTB	Thylacinus cynocephalus cytochrome b...	44	0.001
gb M22450.1 DAVMTCYTB	Dasyurus hallucatus cytochrome b gene...	44	0.001
gb U25737.1 PMU25737	Paradisea minor cytochrome b gene, m...	44	0.001
gb U15203.1 PRU15203	Paradisea rudolphi mitochondrial cyto...	44	0.001
gb U15205.1 PAU15205	Epimachus albertii mitochondrial cyto...	44	0.001
gb U15209.1 PRU15209	Oliphylodes reepublica mitochondrial c...	44	0.001
emb AJ000424.1 STA424	Sorex tundrensis partial mitochondrial...	44	0.001
emb AJ000423.1 STA423	Sorex tundrensis partial mitochondrial...	44	0.001

<a href="#">emb AJ000438.1 STAJ438</a>	Sorex isodon partial mitochondrial c...	44	0.001
<a href="#">emb AJ000437.1 STAJ437</a>	Sorex isodon partial mitochondrial c...	44	0.001
<a href="#">emb AJ000428.1 SAAJ428</a>	Sorex arcticus partial mitochondrial...	44	0.001
<a href="#">emb AJ000427.1 SAAJ427</a>	Sorex arcticus ssp. maritimensis par...	44	0.001
<a href="#">emb AJ000426.1 SAAJ426</a>	Sorex asper partial mitochondrial cy...	44	0.001
<a href="#">emb AJ000425.1 SAAJ425</a>	Sorex asper partial mitochondrial cy...	44	0.001
<a href="#">emb AJ000418.1 SGAJ418</a>	Sorex granarius partial mitochondria...	44	0.001
<a href="#">emb AJ000417.1 SGAJ417</a>	Sorex granarius partial mitochondria...	44	0.001
<a href="#">emb AJ000416.1 SAAJ416</a>	Sorex araneus partial mitochondrial ...	44	0.001
<a href="#">emb AJ004793.1 HCAJ4793</a>	Hippolais caligata ssp. caligata mi...	44	0.001
<a href="#">emb AJ004792.1 HCAJ4792</a>	Hippolais caligata ssp. rama mitoch...	44	0.001
<a href="#">gb U15718.1 RSU15718</a>	Ramphocelus sanguinolentus cytochrome ...	44	0.001
<a href="#">gb L11905.1 CGYMTCYTB0</a>	Cratogeomys gymnurus mitochondrial c...	44	0.001
<a href="#">gb U14679.1 POU14679</a>	Philander opossum cytochrome b light s...	44	0.001
<a href="#">gb L11907.1 CGYMTCYTB1</a>	Cratogeomys goldmani rubellus mitoch...	44	0.001
<a href="#">gb L11906.1 CGYMTCYTB2</a>	Cratogeomys merriami mitochondrial c...	44	0.001
<a href="#">gb L11902.1 CGYMTCYTB3</a>	Cratogeomys castanops castanops mito...	44	0.001
<a href="#">emb X92524.1 SLCYTB</a>	S.longirostris cytochrome b gene (compl...	44	0.001
<a href="#">gb U46771.1 ACU46771</a>	Anthus campestris cytochrome b gene, m...	44	0.001
<a href="#">dbj AB021773.1 AB021773</a>	Anguilla interioris mitochondrial c...	44	0.001
<a href="#">dbj AB006953.1 AB006953</a>	Carassius auratus langsdorfi mitoch...	44	0.001
<a href="#">emb Z73492.1 MTPTTCYTB</a>	P.trochilus mitochondrial cytochrome...	44	0.001
<a href="#">dbj AB035239.1 AB035239</a>	Osteoglossum ferreirai mitochondria...	44	0.001
<a href="#">emb X92532.1 MMCYTB2</a>	M.monoceros cytochrome b gene (complet...	44	0.001
<a href="#">emb X74260.1 MIVOCYTB</a>	V.olivaceus mitochondrion gene for cy...	44	0.001
<a href="#">emb X56293.1 MISLCYTB3</a>	S.longirostris mitochondrion cytb gen...	44	0.001
<a href="#">emb X56292.1 MISLCYTB4</a>	S.longirostris mitochondrion cytb ge...	44	0.001
<a href="#">emb X74256.1 MIPVCYTB</a>	P.violaceus mitochondrion gene for cy...	44	0.001
<a href="#">emb X82304.1 MIPHCYTB3</a>	P.hispida mitochondrial cytochrome b...	44	0.001
<a href="#">emb X82302.1 MIPFCYTB3</a>	P.fasciata mitochondrial cytochrome ...	44	0.001
<a href="#">emb X56284.1 MIOACYTB</a>	O.aries mitochondrion cytb gene for c...	44	0.001
<a href="#">emb X74252.1 MIMKCYTB</a>	M.keraudrenii mitochondrion gene for ...	44	0.001
<a href="#">emb X72005.1 MILWCYTB</a>	L.weddelli mitochondrial gene for cyt...	44	0.001
<a href="#">emb X74259.1 MILLCYTB</a>	L.ludovicianus mitochondrion gene for...	44	0.001
<a href="#">emb Y08814.1 MIHLCYTB3</a>	H.liberiensis mitochondrial cytochro...	44	0.001
<a href="#">emb Y08813.1 MIHACYTB</a>	H.amphibius mitochondrial cytochrome ...	44	0.001
<a href="#">emb X56287.1 MIGCCYTB</a>	G.camelopardalis mitochondrion cytb g...	44	0.001
<a href="#">emb X74253.1 MIEFCYTB</a>	E.fastuosus mitochondrion gene for cy...	44	0.001
<a href="#">emb X60941.1 MIEACB33</a>	Epimachus albertisii mitochondrial ge...	44	0.001
<a href="#">emb X74255.1 MIDMCYTB</a>	D.magnificus mitochondrion gene for c...	44	0.001
<a href="#">emb X56289.1 MICHCYTB</a>	C.hircus mitochondrion cytb gene for ...	44	0.001
<a href="#">emb V00654.1 MISTXX</a>	Bos taurus complete mitochondrial genome	44	0.001
<a href="#">emb X60940.1 MIAMCB33</a>	A.macgregoriae mitochondrial gene for...	44	0.001
<a href="#">emb X92530.1 LACYTB</a>	L.albistrostris cytochrome b gene (comple...	44	0.001
<a href="#">gb U09265.1 CAU09265</a>	Coccyzus americanus mitochondrion cyto...	44	0.001
<a href="#">dbj AB023906.1 AB023906</a>	Petaurista leucogenys mitochondrial...	44	0.001
<a href="#">dbj AB023905.1 AB023905</a>	Petaurista leucogenys mitochondrial...	44	0.001
<a href="#">dbj AB023904.1 AB023904</a>	Petaurista leucogenys mitochondrial...	44	0.001
<a href="#">dbj AB023903.1 AB023903</a>	Petaurista leucogenys mitochondrial...	44	0.001
<a href="#">dbj D88981.1 D88981</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88638.1 D88638</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88636.1 D88636</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88635.1 D88635</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88633.1 D88633</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88632.1 D88632</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88630.1 D88630</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88628.1 D88628</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88627.1 D88627</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D84204.1 GOTMTCB0</a>	Capra aegagrus mitochondrial DNA for ...	44	0.001
<a href="#">dbj D84202.1 GOTMTCB8</a>	Capra falconeri mitochondrial DNA for...	44	0.001
<a href="#">dbj D82893.1 D82893</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D82892.1 D82892</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D82891.1 D82891</a>	Bos javanicus mitochondrial DNA for cyt...	44	0.001
<a href="#">dbj Q12121.1 BBUMTCB2</a>	Bubalus arnee bubalis mitochondrial ...	44	0.001
<a href="#">dbj Q14537.1 BBUMTCB4</a>	Bubalus bubalis mitochondrial gene fo...	44	0.001
<a href="#">dbj AB094974.1 AB094974</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">dbj AB094973.1 AB094973</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">dbj AB094971.1 AB094971</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">dbj AB094952.1 AB094952</a>	Capra aegagrus mitochondrial DNA fo...	44	0.001
<a href="#">dbj D88549.1 D88549</a>	Anoa depressicornis mitochondrial DNA f...	44	0.001
<a href="#">dbj D88537.1 D88537</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001

<a href="#">dbj D88634.1 D88634</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88631.1 D88631</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D88629.1 D88629</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D84205.1 SHPMTCBE</a>	Sheep mitochondrial DNA for cytochrom...	44	0.001
<a href="#">dbj D84203.1 SHPMTCBC</a>	Ovis musimon mitochondrial DNA for cy...	44	0.001
<a href="#">dbj D84201.1 GOTMTCBA</a>	Goat mitochondrial DNA for cytochrome...	44	0.001
<a href="#">dbj D82894.1 D82894</a>	Bubalus bubalis mitochondrial DNA for c...	44	0.001
<a href="#">dbj D82891.1 D82891</a>	Bubalus quarlesi mitochondrial DNA for ...	44	0.001
<a href="#">dbj D14638.1 BBUMTCBB</a>	Bubalus bubalis mitochondrial gene fo...	44	0.001
<a href="#">dbj D14616.1 BOVMTCBB</a>	Bos javanicus mitochondrial gene for ...	44	0.001
<a href="#">dbj AB017602.1 AB017602</a>	Talpa altaica mitochondrial cytb ge...	44	0.001
<a href="#">dbj AB018985.1 AB018985</a>	Cichlasoma citrinellum mitochondria...	44	0.001
<a href="#">dbj AB004075.1 AB004075</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">dbj AB004073.1 AB004073</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">dbj AB004070.1 AB004070</a>	Capra hircus mitochondrial DNA for ...	44	0.001
<a href="#">emb X92531.1 DLCYTB</a>	D.leucas cytochrome b gene (complete se...	44	0.001
<a href="#">gb U07565.1 HAU07565</a>	Hippopotamus amphibius mitochondrion c...	44	0.001
<a href="#">gb U10367.1 PVU10367</a>	Ptilonorhynchus violaceus mitochondrio...	44	0.001
<a href="#">gb U10364.1 CMU10364</a>	Chlamydera maculata mitochondrion cyto...	44	0.001
<a href="#">emb Z96068.1 ASZ96068</a>	Acomys spinosissimus DNA for mitochon...	42	0.005
<a href="#">gb U76507.1 AIU76507</a>	Amblyornis inornatus cytochrome b gene...	40	0.021
<a href="#">gb AF157466.1 AF157466</a>	Lepus timidus cytochrome b (Cyb) gen...	40	0.021
<a href="#">gb AF157464.1 AF157464</a>	Lepus corsicanus haplotype 1 cytochr...	40	0.021
<a href="#">gb AF157463.1 AF157463</a>	Lepus corsicanus haplotype 3 cytochr...	40	0.021
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<a href="#">gb AF265188.1 AF265188</a>	Gillichthys mirabilis cytochrome b m...	40	0.021
<a href="#">gb AF324034.1 AF324034</a>	Phyllobates aurotaenia isolate Quebr...	40	0.021
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<a href="#">gb AF272633.1 AF272633</a>	Clethrionomys gapperi specimen-vouch...	40	0.021
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<a href="#">gb AF155385.1 AF155385</a>	Peromyscus attwateri isolate 1b cyto...	40	0.021
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<a href="#">gb AF155520.1 AF155520</a>	Sigmodon ochrognathus isolate Duran4...	40	0.021
<a href="#">gb AF155519.1 AF155519</a>	Sigmodon ochrognathus isolate Elam8...	40	0.021
<a href="#">gb AF155518.1 AF155518</a>	Sigmodon ochrognathus isolate Bbend4...	40	0.021
<a href="#">gb AF133531.1 AF133531</a>	Trachyphonus darnaudii cytochrome b ...	40	0.021
<a href="#">gb AF254947.1 AF254947</a>	Urocyon v. leucurus cytochrome b gene. co...	40	0.021
<a href="#">gb AF205531.1 AF205531</a>	Podarcis sicula cytochrome b gene. p...	40	0.021
<a href="#">gb AF123705.1 AF123705</a>	Hippocampus zosterae haplotype FK.14...	40	0.021
<a href="#">ccl NC 000994.1 </a>	Cavia porcellus complete mitochondrial genome	42	0.021

<u>gb AF004572.1 AF004572</u>	Arvicanthus niloticus cytochrome b (...)	<u>40</u>	0.021
<u>gb AF088932.1 AF088932</u>	Sminthopsis psammophila cytochrome b...	<u>40</u>	0.021
<u>gb U62697.1 ORUCYT82</u>	Oreopholus ruficollis cytochrome b (cy...	<u>40</u>	0.021
<u>gb U62681.1 CACYT82</u>	Charadrius australis cytochrome b (cyt ...)	<u>40</u>	0.021
<u>gb U62707.1 CVERCYT82</u>	Charadrius veredus cytochrome b (cytb...	<u>38</u>	0.084
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## Alignments

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<u>AF081959</u>	872	.....c.....	847
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<u>AF144313</u>	161	.....g.....	136
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<u>AF144311</u>	161	.....g.....	136
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<u>AF144309</u>	161	.....g.....	136
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<u>AF290132</u>	752	.....g.....	727
<u>NC 002504</u>	15022	.....g.....	14997
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<u>AF119261</u>	869	.....g.....	844
<u>AF119259</u>	869	.....g.....	844
<u>AF288454</u>	91	.....a.....	66
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<u>AF123647</u>	68	.....g.....	43
<u>AF123646</u>	104	.....g.....	77
<u>AF123643</u>	68	.....g.....	43
<u>AF123644</u>	84	.....g.....	59

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<u>AF123618</u>	104	.....g.....	79
<u>AF123614</u>	104	.....g.....	79
<u>AF123613</u>	101	.....g.....	76
<u>AF127201</u>	107	.....g.....	82
<u>AF127192</u>	107	.....c.....	82
<u>AF127189</u>	107	.....g.....	82
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<u>NC 001610</u>	15045	.....c.....	15020
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<u>AF168758</u>	507	.....a.....	482
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<u>AF059054</u>	776	.....c.....	751
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<u>AF160611</u>	238	.....g.....	213
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<u>AF160604</u>	869	.....g.....	844
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Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 19068

Number of Sequences: 807597

Number of extensions: 19068

Number of successful extensions: 7580

Number of sequences better than 10.0: 2441

length of query: 26

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 9

effective length of database: 2,850,098,736

effective search space: 25650888624

effective search space used: 25650888624

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

**Table 12.** The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
1.	Indian black buck no.1
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile no1
10	crocodile no2
11	turtle no1
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird no1
21	weaver bird no2
22	buffalo no1
23	buffalo no 2

## CLAIMS

- 1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name	Sequence (5'-3')
mcb 398	"TACCATGAGGACAAATATCATTCTG"
mcb 869	"CCTCCTAGTTTGTTAGGGATTGATCG"

2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.
3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.
4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.
5. Primers as claimed in claim 1 wherein in *Antelope cervicapra* species, the sequences of the fragment mentioned under claim 1 are as follows:
- Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antelope cervicapra*:
- "taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatatcggtacaaacctag tagaatgaatctgaggagggttctcagtagataaagcaaccctacccgattttcgcttccactttatctcccatttatcattgc agcccttaccatagtagacactactgtttctccacgaaacaggatccaacaacccccacaggaatctcatcagacgcagacaaa attccattccacccctactacactatcaaagatctcctaggagctctactattaattttaaccctcatgcttctagtcctattctcacc ggacctgcttgagagaccagacaactatacaccagcaaaccacttaatacacccccacatatcaagcccgaatgatacttc ctatttgcatagcgaatcctccgatcaattcctaacaaactaggagg"
6. A method for the identification of the animal from a biological sample, said method comprising the steps of:
- isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
  - sequencing the amplified products,
  - blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample.

- d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,
- 5 e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,
- f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,
- 10 g) aligning the sequences obtained using CLUSTRAL program and identifying the variable sites amongst the animals analyzed,
- h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal
- 15 of the biological sample.
7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.
- 20 8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ng of template DNA, 100µM each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl<sub>2</sub>, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35<sup>th</sup> cycles should be held for 10 min.
- 25 9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.
- 30 10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.
11. A method as claimed in claim 6 wherein the method is used to establish the identity of

biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

- 5 12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.
13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
- 10 14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
- 15 15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
- 20 16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECULAR KIT' and (b) 'DNA CHIPS' based applications for wildlife identification in forensics.

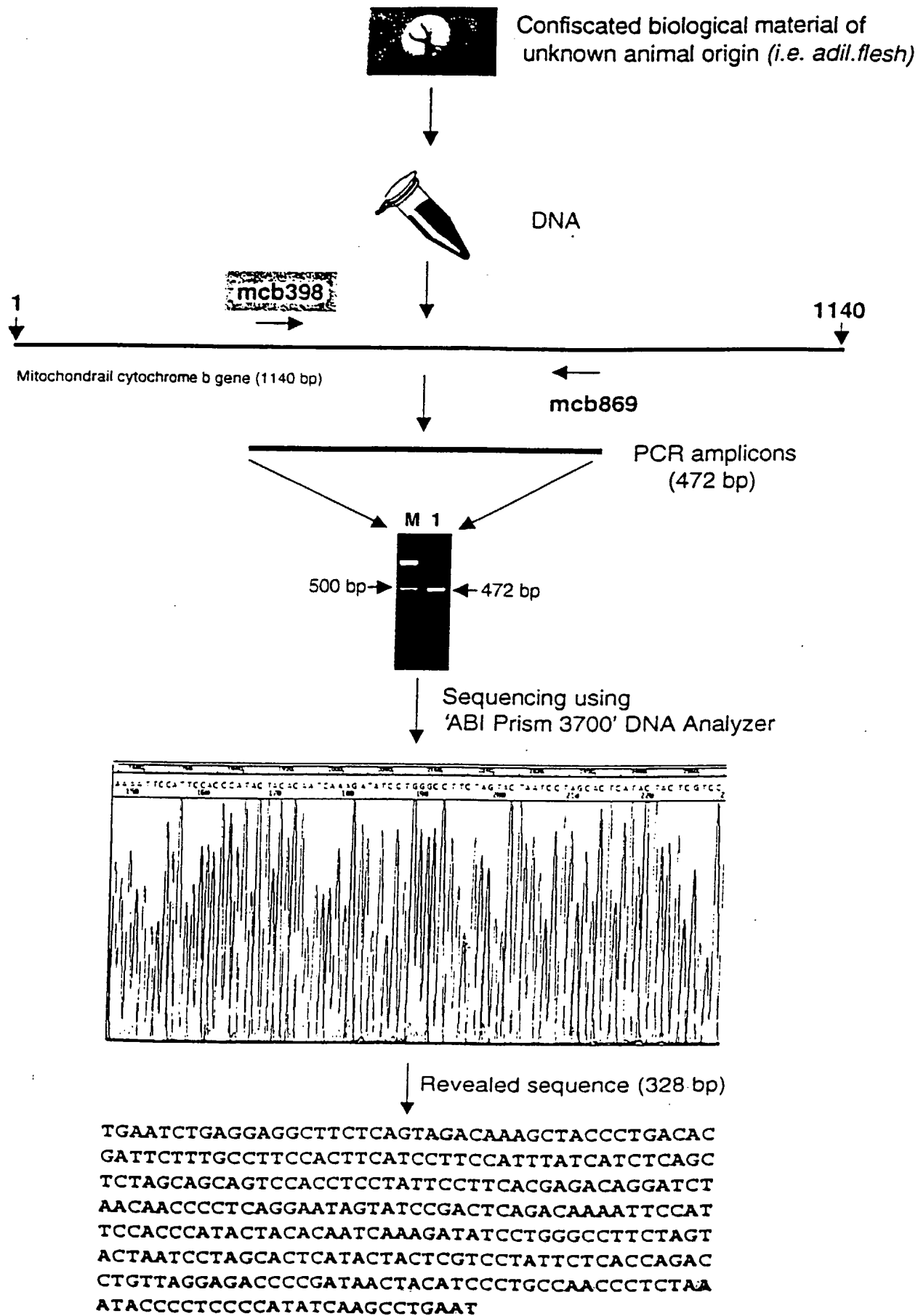


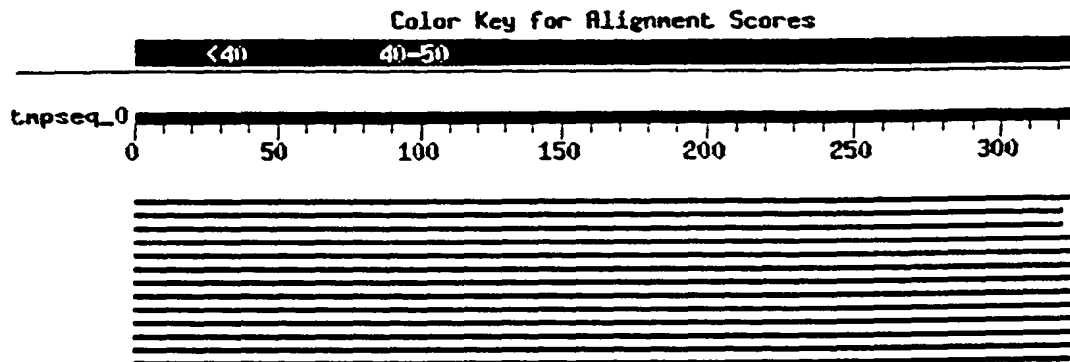
Figure 1 a



Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. '*adil.flesh*' using primers 'mcb398' and 'mcb869'

Homology search in '*nr*' database using '*BLAST*'

<http://www.ncbi.nlm.nih.gov/BLAST/>



Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1  <i>Panthera pardus</i> cytochrome b gene, partial c...	603	e-170
gb AF053054.1 AF053054 <i>Panthera tigris sumatrae</i> isolate Su1...	527	e-147
gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi...	527	e-147
gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 ...	476	e-132
gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1 ...	476	e-132

Selection of reference animals based on above information  
and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments  
using '*Autoassembler*'

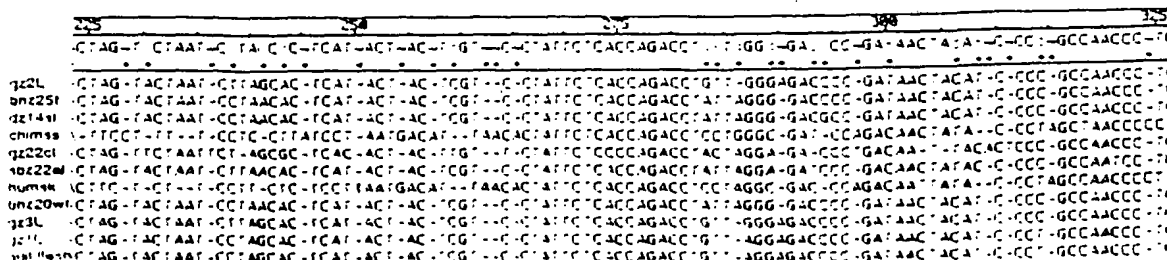


Figure 1 b

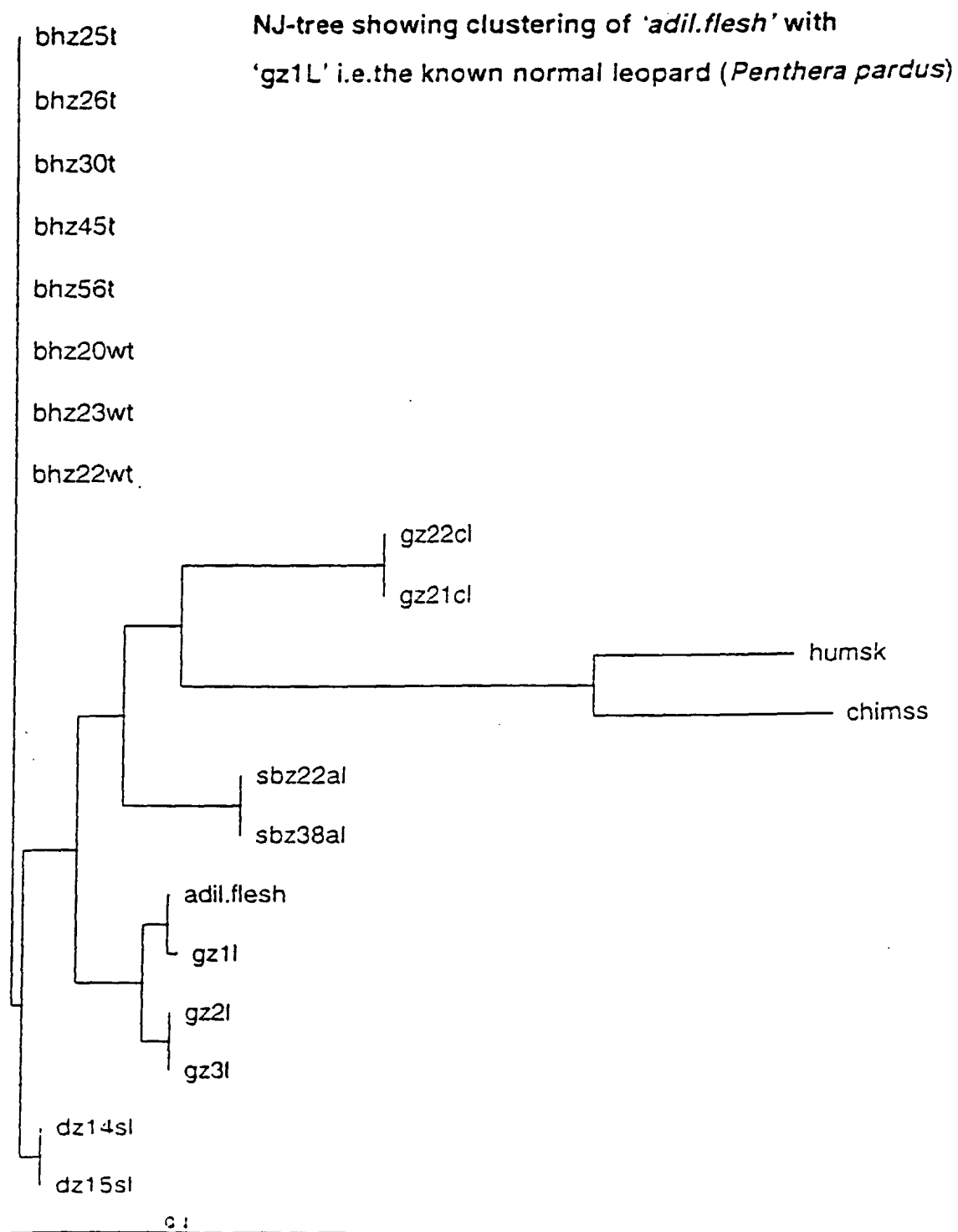


Figure 1c

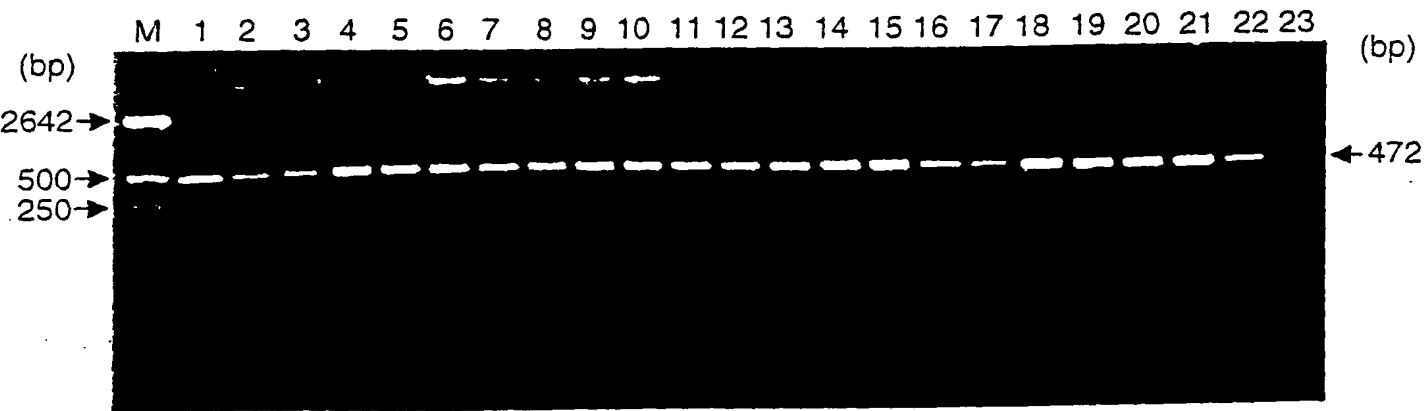


Figure 2

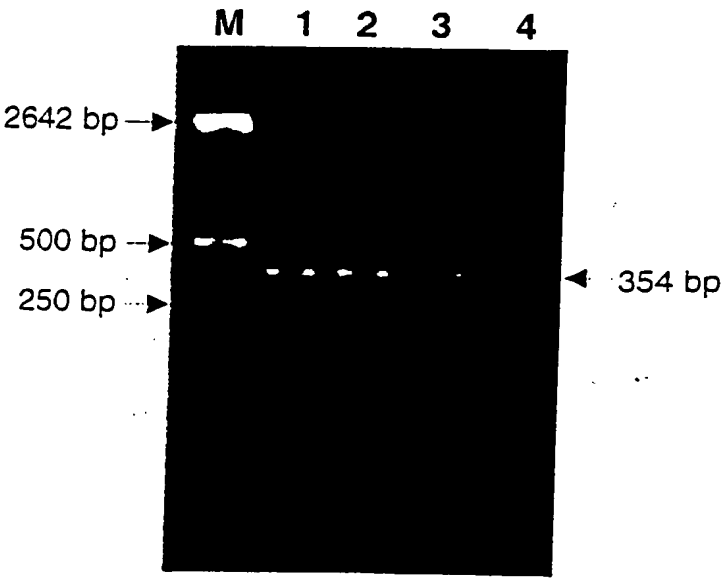


Figure 3

6/6

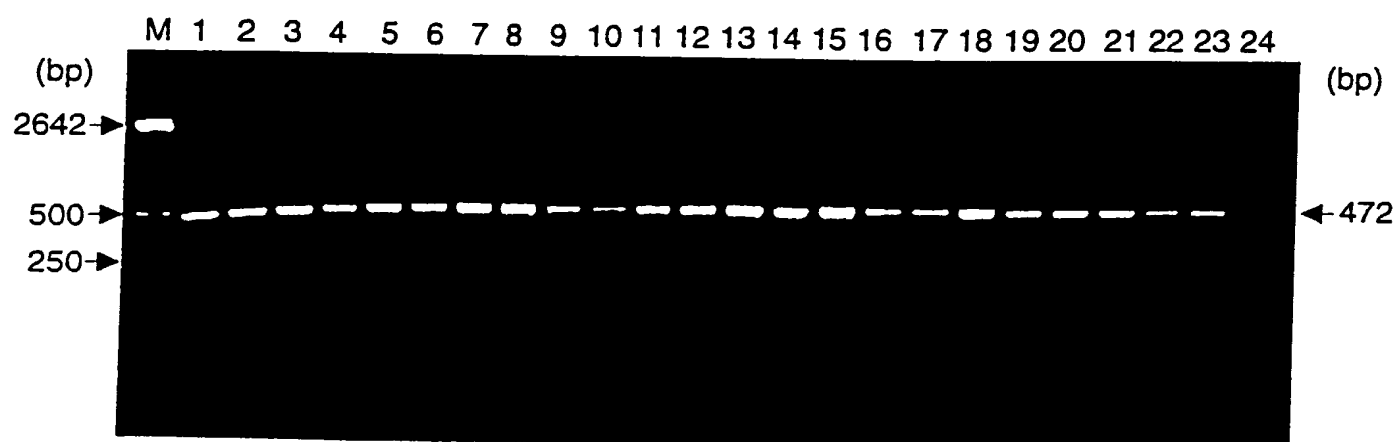


Figure 4

## INTERNATIONAL SEARCH REPORT

Inte Application No  
PC 1 / 1 IN 01/00055

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KOCHER T D ET AL: "DYNAMICS OF MITOCHONDRIAL DNA EVOLUTION IN ANIMALS AMPLIFICATION AND SEQUENCING WITH CONSERVED PRIMERS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 86, no. 16, 1989, pages 6196-6200, XP002189444 1989 ISSN: 0027-8424 the whole document ---	1-16
Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT ;BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document --- -/--	1-16

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## ° Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
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- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*G\* document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

12/03/2002

Name and mailing address of the ISA

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Authorized officer

Hagenmaier, S

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/IN 01/00055

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	IRWIN D M ET AL: "EVOLUTION OF THE CYTOCHROME BETA GENE OF MAMMALS" JOURNAL OF MOLECULAR EVOLUTION, SPRINGER VERLAG, NEW YORK, NY, US, vol. 2, no. 3, June 1995 (1995-06), pages 128-144, XP000892117 ISSN: 0022-2844 the whole document ---	1-16
Y	DATABASE EMBL 'Online! ID/AC AAF56513, 28 November 2000 (2000-11-28) ZH NIPPON KAGAKU SENI KENSA KYOKAI: "Animal fibre identification PCR primer #3" XP002191314 abstract ---	1-16
Y	WO 93 15215 A (HYDROCARBON RESEARCH INC) 5 August 1993 (1993-08-05) the whole document ---	1-16
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